

# SEARCH REQUEST FORM

## Scientific and Technical Information Center

Requester's Full Name: \_\_\_\_\_ Examiner #: \_\_\_\_\_ Date: \_\_\_\_\_

Art Unit: \_\_\_\_\_ Phone Number 30 \_\_\_\_\_ Serial Number: \_\_\_\_\_

Mail Box and Bldg/Room Location: \_\_\_\_\_ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

\*\*\*\*\*

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: \_\_\_\_\_

Inventors (please provide full names): \_\_\_\_\_

Earliest Priority Filing Date: \_\_\_\_\_

\*For Sequence Searches Only\* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

STAFF USE ONLY		Type of Search	Vendors and cost where applicable
Searcher:	If Contact: <b>Sheppard</b>	NA Sequence (#)	STN _____
Searcher Phone #:		AA Sequence (#)	Dialog _____
Searcher Location:	101: 305-4499	Structure (#)	Questel/Orbit _____
Date Searcher Picked Up:	1/1/1	Bibliographic	Dr. Link _____
Date Completed		Litigation	Lexis/Nexis _____
Searcher Prep & Review Time		Fulltext	Sequence Systems _____
Clencal Prep Time		Patent Family	WWW/Internet _____
Online Time.		Other	Other (specify) _____



RESULT 2  
US-08-915-795-8  
Sequence 8, Application US/08915795  
Patent No. 6235713  
GENERAL INFORMATION:  
APPLICANT: Marc G. ACHEN  
APPLICANT: Andrew F. WILKS  
APPLICANT: Steven A. STACKER  
APPLICANT: Kari ALITALO  
TITLE OF INVENTION: GROWTH FACTOR  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.  
STREET: 1200 G Street, NW, Suite 700  
CITY: Washington  
STATE: DC  
COUNTRY: United States of America  
ZIP: 20005  
COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/915,795  
FILED DATE: 08/08/1997  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: EVANS, JOSEPH D.  
REGISTRATION NUMBER: 26,269  
REFERENCE/DOCKET NUMBER: 1064/42983  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 628-8800  
TELEFAX: (202) 628-8844  
TELEX: N/A  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 325 amino acids  
STRANDEDNESS: single  
TOPOLogy: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
TISSUE TYPE: Human Breast  
US-08-915-795-3

Query Match 19.2%; Score 119.5; DB 4; Length 358;  
Best Local Similarity 33.3%; Pred. No. 1.5e-05;  
Matches 36; Conservative 15; Mismatches 42; Indels 15; Gaps 6;

QY 4 LNLITBEVRVLYSCTPRNFSVIREEL-KRDTTIFPGCLLVKRCGGNCACCLHNCNECQC 62  
Db 104 LKVIBEWQRCQSPRETCVEVASLGKSTNTFFKPPCVNFRCCG--CC--NBEQVMC 153  
QY 63 V--PSKVTKYHEVQLRPLRKVGGLHKSLLTDVALEHHBECDCV 107  
Db 159 MNTSISYISKOLFESV--PLTSV---PELVPKVIANHGTGCKCLPTG 200

RESULT 3  
US-08-915-795-3  
Sequence 3, Application US/08915795  
Patent No. 6235713  
GENERAL INFORMATION:  
APPLICANT: Marc G. ACHEN  
APPLICANT: Andrew F. WILKS  
APPLICANT: Steven A. STACKER  
APPLICANT: Kari ALITALO  
TITLE OF INVENTION: GROWTH FACTOR  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.  
STREET: 1200 G Street, NW, Suite 700  
CITY: Washington

Patent No. 6235713  
GENERAL INFORMATION:  
APPLICANT: Marc G. ACHEN  
APPLICANT: Andrew F. WILKS  
APPLICANT: Steven A. STACKER  
APPLICANT: Kari ALITALO  
TITLE OF INVENTION: GROWTH FACTOR  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.  
STREET: 1200 G Street, NW, Suite 700  
CITY: Washington  
STATE: DC  
COUNTRY: United States of America  
ZIP: 20005  
COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/915,795  
FILED DATE: 08/08/1997  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: EVANS, JOSEPH D.  
REGISTRATION NUMBER: 26,269  
REFERENCE/DOCKET NUMBER: 1064/42983  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 628-8800  
TELEFAX: (202) 628-8844  
TELEX: N/A  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 325 amino acids  
STRANDEDNESS: single  
TOPOLogy: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
TISSUE TYPE: Human Breast  
US-08-915-795-3

Query Match 18.6%; Score 115.5; DB 4; Length 325;  
Best Local Similarity 33.0%; Pred. No. 3.8e-05;  
Matches 34; Conservative 14; Mismatches 44; Indels 11; Gaps 5;

QY 4 LNLITBEVRVLYSCTPRNFSVIREEL-KRDTTIFPGCLLVKRCGGNCACCLHNCNECQ-0 61  
Db 70 LKVIBEWQRCQSPRETCVEVASLGKSTNTFFKPPCVNFRCCG--CC--NCENEESLICM 126  
QY 62 CVPSKVTKYHEVQLRPLRKVGGLHKSLLTDVALEHHBECDCV 104  
Db 127 TSTSYISKOLFESV--PLTSV---PELVPKVIANHGTGCKCLPTG 163

RESULT 4  
US-08-915-795-5  
Sequence 5, Application US/08915795  
Patent No. 6235713  
GENERAL INFORMATION:  
APPLICANT: Marc G. ACHEN  
APPLICANT: Andrew F. WILKS  
APPLICANT: Steven A. STACKER  
APPLICANT: Kari ALITALO  
TITLE OF INVENTION: GROWTH FACTOR  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.  
STREET: 1200 G Street, NW, Suite 700  
CITY: Washington

COUNTRY: United States of America  
 ZIP: 20005  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, version #1.25  
 CURRENT APPLICATION DATA:  
 CURRENT APPLICATION NUMBER: US/08/915,795  
 FILING DATE: 24-JAN-1992  
 CLASSIFICATION: 536  
 ATTORNEY/AGENT INFORMATION:  
 NAME: EVANS, Joseph D.  
 REGISTRATION NUMBER: 26,269  
 REFERENCE/DOCKET NUMBER: 10644-2983  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 628-8800  
 TELEFAX: (202) 628-8844  
 TELEX: N/A  
 INFORMATION FOR SEQ ID NO: 5:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 354 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 HYPOTHETICAL: NO  
 ORIGINAL SOURCE:  
 TISSUE TYPE: Human Lung  
 LT 5  
 8-094-079-2  
 156 TTSYVSKOLFELISV-PLTSV---PELVPKVANHPTGCKCL 192  
 query sequence 2, Application US/08094079  
 general information:  
 applicant: COOK, Anne L  
 applicant: CRAIG, Stewart  
 applicant: CLEMENTS, John M  
 applicant: EDWARDS, Richard M  
 applicant: BROWN, David  
 title of invention: PDGF-B ANALOGUES  
 number of sequences: 22  
 correspondence address:  
 addressee: Allegretti & Witcoff, Ltd.  
 street: 10 S. Wacker Dr.  
 city: Chicago  
 state: Illinois  
 country: USA  
 zip: 60606  
 computer readable form:  
 medium type: Floppy disk  
 computer: IBM PC compatible  
 operating system: PC-DOS/MS-DOS  
 software: Patent In Release #1.0, version #1.25  
 current application data:  
 application number: US/08/915,795  
 filing date: 24-JAN-1992  
 classification: 435  
 prior application data:  
 application number: WO PCT/GB92/00141  
 filing date: 24-JAN-1992  
 prior application data:  
 application number: GB 9101645.1  
 filing date: 24-JAN-1991  
 attorney/agent information:  
 name: McDonnell, John J  
 registration number: 26,949  
 reference/docket number: 93,640  
 telecommunication information:  
 telephone: 312-715-1000  
 telefax: 312-715-1234  
 information for seq id no: 2:  
 sequence characteristics:  
 length: 109 amino acids  
 type: amino acid  
 strandedness: single  
 topology: linear  
 molecule type: protein  
 name/key: Protein  
 location: 1..109  
 other information: /note= "Truncated PDGF-B (PDGF-Bt)"  
 LT 5  
 8-094-079-2  
 query sequence 3, Application US/08094079  
 general information:  
 patent no. 5512545  
 general information:  
 applicant: COOK, Anne L  
 applicant: CRAIG, Stewart  
 applicant: CLEMENTS, John M  
 applicant: EDWARDS, Richard M  
 applicant: BROWN, David  
 title of invention: PDGF-B ANALOGUES  
 number of sequences: 22  
 correspondence address:  
 addressee: Allegretti & Witcoff, Ltd.  
 street: 10 S. Wacker Dr.  
 city: Chicago  
 state: Illinois  
 country: USA  
 zip: 60606  
 computer readable form:  
 medium type: Floppy disk  
 computer: IBM PC compatible  
 operating system: PC-DOS/MS-DOS  
 software: Patent In Release #1.0, version #1.25  
 current application data:  
 application number: US/08/915,795  
 filing date: 24-JAN-1992  
 classification: 435  
 prior application data:  
 application number: WO PCT/GB92/00141  
 filing date: 24-JAN-1992  
 prior application data:

APPLICATION NUMBER: GB 9101645.1  
 FILING DATE: 24-JAN-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: McConnell, John J  
 REGISTRATION NUMBER: 26,949  
 REFERENCE/DOCKET NUMBER: 93,640  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 312-715-1000  
 TELEFAX: 312-715-1234  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 109 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 FEATURE:  
 NAME/KEY: Protein  
 LOCATION: 1..109  
 OTHER INFORMATION: /note= "truncated PDGF-B with ARG  
 OTHER INFORMATION: 28 > SER (PDGF-B5)"  
 US-08-094-079-3

Query Match 16.9%; Score 105; DB 1; Length 109;  
 Best Local Similarity 33.3%; Pred. No. 0.00015; Indels 36; Gaps 9;  
 Matches 36; Conservative 12; Mismatches 34; Index 26; Gaps 9;

QY 7 LTEEVRLYSCTPRN-FSVSIREEKRTDTIF-WPGCLVKRQGGNCACCLHNCNECQC 62  
 Db 7 IAEPMIAECKTRTEVFEFS-RSLIDRTNANFLWMPPCVEVORSGG--CC--NNRNQOC 60  
 GENERAL INFORMATION:  
 APPLICANT: Hoppe, Jürgen  
 APPLICANT: Welch, Herbert  
 TITLE OF INVENTION: PDGF-A, PDGF-AB, PREPARATION PROCESS AND  
 TITLE OF INVENTION: PHARMACEUTICALS CONTAINING  
 TITLE OF INVENTION: THEM  
 NUMBER OF SEQUENCES: 3

RESULT 7  
 US-08-804-953-3

QY 7 LTEEVRLYSCTPRN-FSVSIREEKRTDTIF-WPGCLVKRQGGNCACCLHNCNECQC 62  
 Db 7 IAEPMIAECKTRTEVFEFS-RSLIDRTNANFLWMPPCVEVORSGG--CC--NNRNQOC 60  
 GENERAL INFORMATION:  
 APPLICANT: Hoppe, Jürgen  
 APPLICANT: Welch, Herbert  
 TITLE OF INVENTION: PDGF-A, PDGF-AB, PREPARATION PROCESS AND  
 TITLE OF INVENTION: PHARMACEUTICALS CONTAINING  
 TITLE OF INVENTION: THEM

NUMBER OF SEQUENCES: 3

RESULT 7  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Joseph T. Eisele

ADDRESSEE: Kane, Dalsimer, Sullivan, Kurucz,  
 ADDRESSEE: Levy, Eisele and Richard  
 STREET: 711 Third Avenue

CITY: New York  
 STATE: New York  
 COUNTRY: U.S.A.

ZIP: 10017-4059

COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3-1/2" DISKETTE  
 COMPUTER: IBM-XT COMPATIBLE  
 OPERATING SYSTEM: DOS 3.3;  
 SOFTWARE: WORDPERFECT 5.0

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/804, 953  
 FILING DATE: 24-FEB-1997  
 CLASSIFICATION: 257

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/720,771  
 FILING DATE: 08/07/91  
 APPLICATION NUMBER: PCT/EP90/00063  
 FILING DATE: 01/11/90

ATTORNEY/AGENT INFORMATION:

NAME: EISELE, JOSEPH T.  
 REGISTRATION NUMBER: 25,331  
 REFERENCE/DOCKET NUMBER: 2727-56 PCT  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 687-6000  
 TELEFAX: (212) 682-4885  
 TELEX: (212) 456767  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 109 residues  
 TYPE: amino acid  
 STRANDEDNESS: N/A  
 TOPOLOGY: linear  
 MOLECULE TYPE: Protein  
 HYPOTHETICAL: Yes  
 ANTI-SENSE: No  
 FRAGMENT TYPE:  
 ORIGINAL SOURCE:  
 ORGANISM:  
 STRAIN: E. coli  
 INDIVIDUAL ISOLATE:  
 DEVELOPMENTAL STAGE:  
 HAPLOTYPE:  
 TISSUE TYPE:  
 CELL TYPE:  
 CELL LINE:  
 ORGANELLE:  
 IMMEDIATE SOURCE:  
 CLONE: PDGF-A  
 FEATURE:  
 OTHER INFORMATION:  
 US-08-804-953-3

Query Match 16.9%; Score 105; DB 2; Length 109;  
 Best Local Similarity 33.3%; Pred. No. 0.00015; Indels 36; Gaps 9;

QY 7 LTEEVRLYSCTPRN-FSVSIREEKRTDTIF-WPGCLVKRQGGNCACCLHNCNECQC 62  
 Db 7 IAEPMIAECKTRTEVFEFS-RSLIDRTNANFLWMPPCVEVORSGG--CC--NNRNQOC 60  
 GENERAL INFORMATION:  
 APPLICANT: Kejt, Bruce A.  
 APPLICANT: Nguyen, Francis H.  
 APPLICANT: Ferrara, Napoleone  
 APPLICANT: Cunningham, Brian C.  
 APPLICANT: Weils, James A.  
 APPLICANT: Li, Bing

TITLE OF INVENTION: Variants of Vascular Endothelial Cell  
 TITLE OF INVENTION: Growth Factor, Their Uses, and Processes for their  
 TITLE OF INVENTION: Production

NUMBER OF SEQUENCES: 45

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Flehr, Hobnach, Test, Albritton & Herbert  
 STREET: Four Embarcadero Center, Suite 3400  
 CITY: San Francisco  
 STATE: California  
 COUNTRY: United States  
 ZIP: 94111-4167

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/691,794  
 FILING DATE: 02-AUG-1996  
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/002,827  
 FILING DATE: 25-AUG-1995  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 08/567,200  
 FILING DATE: 05-DEC-1995

ATTORNEY/AGENT INFORMATION:  
 NAME: Dreyer, Walter H.  
 REGISTRATION NUMBER: 24,1190  
 REFERENCE/DOCKET NUMBER: A-63758/NHD  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 781-1989  
 TELEFAX: (415) 398-3249  
 TELEX: 910 277299  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 109 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: unknown  
 TOPOLOGY: unknown  
 MOLECULE TYPE: protein  
 US-08-691-794-4

Query Match 16.9%; Score 105; DB 3; Length 109;  
 Best Local Similarity 33.3%; Pred. No. 0.00015; DB 3; Length 109;  
 Matches 36; Conservative 12; Mismatches 34; Indels 26; Gaps 9;  
 Qy 7 LTEEVRLYSCPRN-FSVSIREELKRTDTF--WPGCLLVRGGNCACCLHNCBQC 62  
 Db 7 IAEPAAMIAECKTRTEVFEIS-RRLIDRTANFLVWPPCVCVERCSG--CC--NNRNVQC 60  
 Qy 63 VPSKVTKYHEVQLRP---KTGV--RGLHKSLSLDALEHHEEDC 103  
 Db 61 RPTQV-----QLRQVQVRIEIVRKKPITKKAT-VTLEDHACKC 99

RESULT 10  
 PCT-US93-02612-1  
 Sequence 1, Application PC/TUS9302612  
 GENERAL INFORMATION:  
 APPLICANT: Cable, Michael  
 APPLICANT: Hesson, Thomas  
 APPLICANT: Mannarino, Anthony  
 TITLE OF INVENTION: Monomeric Platelet-Derived Growth Factor and Prevention of  
 NUMBER OF SEQUENCES: 8  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Schering-Plough Corporation  
 STREET: One Giralta Farms  
 CITY: Madison  
 STATE: New Jersey  
 COUNTRY: USA  
 ZIP: 07940

RESULT 9  
 PCT-US91-02766-18  
 Sequence 18, Application PC/TUS9102766  
 GENERAL INFORMATION:  
 APPLICANT: NASCIMENTO, CARLOS G.  
 APPLICANT: CALDERON-CACIA, MARIA D.  
 TITLE OF INVENTION: GLYCOSYLATED PDGF  
 NUMBER OF SEQUENCES: 24  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Irail & Manella  
 STREET: 545 Middlefield Road, Suite 200  
 CITY: Menlo Park  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94025

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: Apple Macintosh  
 OPERATING SYSTEM: Macintosh 6.0.5  
 SOFTWARE: Microsoft Word 4.00B  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT-US93/02612  
 FILING DATE: 19930326  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA: None  
 NAME: Lunn, Paul, G.  
 REGISTRATION NUMBER: 32,743  
 REFERENCE/DOCKET NUMBER: JBO255  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 201-822-7255  
 TELEFAX: 201-822-7259  
 TELEX: 219165

Query Match 16.9%; Score 105; DB 5; Length 109;  
 Best Local Similarity 33.3%; Pred. No. 0.00015; DB 5; Length 109;  
 Matches 36; Conservative 12; Mismatches 34; Indels 26; Gaps 9;  
 Qy 1 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 109 amino acids  
 TYPE: AMINO ACID  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 PCT-US93-02612-1

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/515,474  
 FILING DATE: 26-APR-1990  
 ATTORNEY/AGENT INFORMATION:  
 NAME: ROBINS, ROBERT L.  
 REGISTRATION NUMBER: 33,208  
 REFERENCE/DOCKET NUMBER: 2300-0105-40



Sequence 2, Application US/08989251  
 PATENT No. 601731

## GENERAL INFORMATION:

APPLICANT: Tekamp-Olson, Patricia

TITLE OF INVENTION: METHOD FOR EXPRESSION OF HETEROLOGOUS PROTEINS IN YEAST

NUMBER OF SEQUENCES: 41

CORRESPONDENCE ADDRESS: Bell Seltzer IP Group of Alston &amp; Bird, LLP

STREET: 3605 Glenwood Ave. Suite 310

CITY: Raleigh

STATE: NC

COUNTRY: US

ZIP: 27622

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/989,251

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Spruill, W. Murray

REGISTRATION NUMBER: 32,943

REFERENCE/DOCKET NUMBER: 5784-4

TELECOMMUNICATION INFORMATION:

TELEPHONE: 919 420 2202

TELEFAX: 919 881 3175

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

SEQUENCE FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 146 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-989-251-2

Query Match 16.9%; Score 105; DB 3; Length 146;  
 Best Local Similarity 33.3%; Pred. No. 0.00021; Gaps 9;  
 Matches 36; Conservative 12; Mismatches 34; Indels 26; Gaps 9;  
 Name: Spruill, W. Murray  
 Registration Number: 32,943  
 Reference/Docket Number: 5784-4

Query Match 16.9%; Score 105; DB 3; Length 146;  
 Best Local Similarity 33.3%; Pred. No. 0.00021; Gaps 9;  
 Matches 36; Conservative 12; Mismatches 34; Indels 26; Gaps 9;

Qy 7 LTEEVRLVSTCPRN--FSVSVIREELKRTDTIF--WPGCLLVRKGGNACCLHNCNECQC 62  
 Db 44 IAPAMIAECKTRTEVFEIS-RRLIDRINANFLWPPCVCVERCSCG--CC--NNRNQQC 97

Qy 63 VPSKVTKVHEVQLRP---KIGV--RGLHKSLSLTDVALEHHEEDC 103  
 Db 98 RPRQV-----QLRPVQVRKIEIVRKPIFKKAT-VTLEDHLACKC 136

Qy 7 LTEEVRLVSTCPRN--FSVSVIREELKRTDTIF--WPGCLLVRKGGNACCLHNCNECQC 62  
 Db 44 IAPAMIAECKTRTEVFEIS-RRLIDRINANFLWPPCVCVERCSCG--CC--NNRNQQC 97

Qy 63 VPSKVTKVHEVQLRP---KIGV--RGLHKSLSLTDVALEHHEEDC 103  
 Db 98 RPRQV-----QLRPVQVRKIEIVRKPIFKKAT-VTLEDHLACKC 136

Search completed: July 3, 2001, 10:29:37  
 Job time: 237 sec

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/989,251  
 FILING DATE:  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Spruill, W. Murray  
 REGISTRATION NUMBER: 32,943  
 REFERENCE/DOCKET NUMBER: 5784-4

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 919 420 2202  
 TELEFAX: 919 881 3175

INFORMATION FOR SEQ ID NO: 25:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 146 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein

US-08-989-251-25

RESULT 15  
 US 08-989-251-25  
 Sequence 25, Application US/08989251  
 Patent No. 601731

GENERAL INFORMATION:  
 APPLICANT: Tekamp-Olson, Patricia  
 TITLE OF INVENTION: METHOD FOR EXPRESSION OF HETEROLOGOUS PROTEINS IN YEAST  
 NUMBER OF SEQUENCES: 41  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Bell Seltzer IP Group of Alston & Bird, LLP  
 STREET: 3605 Glenwood Ave. Suite 310  
 CITY: Raleigh  
 STATE: NC  
 COUNTRY: US  
 ZIP: 27622

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30



CC regulator. An antisense molecule of the invention is useful for treating  
CC or preventing cancer, rheumatoid arthritis, psoriasis and diabetic  
CC retinopathy by inhibiting angiogenic activity or inappropriate  
CC vascularization including formation and proliferation of new blood  
CC vessels, growth and development of tissues, tissue regeneration and organ  
CC and tissue repair in a subject. The products of the invention are useful  
CC for preparing medicaments for treating wounds such as dermal ulcers,  
CC pressure sores, venous sores, diabetic ulcers and burns and to promote  
CC skin graft growth, tissue repair, proliferation of new blood vessels,  
CC tissue regeneration and organ repair by promoting angiogenic activity or  
CC vascularization. This sequence represents the human 990126vegx protein  
CC used to illustrate the method of the invention.

XX Sequence 345 AA;

Query Match 100.0%; Score 621; DB 21; Length 345;  
Best Local Similarity 100.0%; Pred. No. 4.7e-57;  
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 WVDNLILTEEVRLISCTPRNFSVIREEKRTDTFWPGCLLVRGGNCACCHNCNEC 60  
Db 235 vvdnlilteevrlisctprnfsvireekrtdtfwpgcllvrccgnaccihnc 294  
Qy 61 QCVVSKVTKYHEVQLRKRTGVLHKLTDVALLERHEECDVCVRGSGGG 111  
Db 295 qcvvskvtkyhevqlrkrtgvlhkltdvallerheecdvcvrgstgg 345

Search completed: July 3, 2001, 10:29:13  
Job time: 313 sec

## GenCore version 4.5

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Om protein - protein search, using sw model

Run on: July 3, 2001, 10:29:40 ; Search time 9.84 Seconds

(without alignments) 386.419 Million cell updates/sec

Title: US-09-541-752-2\_COPY\_235\_345

Perfect score: 621

Sequence: 1 VWDLNLLTEEVRLYSLCIPRN. .... DVALEHHECDCVCRGSGTGG 111

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255466 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No. Score Query Length DB ID Description

1 114.5 18.4 148 1 VEGF\_ORFN7

2 108.5 17.5 164 1 VEGF\_CAYPO

3 108.0 17.4 213 1 VEGF\_RABIT

4 105.0 16.9 188 1 VEGF\_HUMAN

5 105.0 16.9 226 1 PDCA\_XENIA

6 105.0 16.9 241 1 PDCH\_HUMAN

7 105.0 16.9 245 1 PDGB\_FELCA

8 104.5 16.8 215 1 VEGF\_HUMAN

9 104.0 16.7 204 1 PDCA\_RAT

10 104.0 16.7 211 1 PDCA\_HUMAN

11 104.0 16.7 211 1 PDCA\_MOUSE

12 104.0 16.7 226 1 TSIS\_SMAY

13 102.5 16.5 133 1 VEGF\_OREN

14 102.5 16.5 190 1 VEGF\_PIG

15 102.5 16.5 419 1 VEGF\_HUMAN

16 101.5 16.3 190 1 VEGF\_BOVIN

17 101.5 16.3 415 1 VEGC\_MOUSE

18 101.5 16.3 196 1 VEGC\_MOUSE

19 96.5 15.5 190 1 VEGF\_RAT

20 95.5 15.4 214 1 VEGF\_MOUSE

21 95.0 15.1 225 1 PDGB\_RAT

22 94.0 15.1 241 1 PDGB\_MOUSE

23 94.0 15.1 216 1 VEGF\_CHICK

24 88.5 14.3 216 1 PDGB\_SHEEP

25 87.0 14.0 241 1 PLGF\_MOUSE

26 84.0 13.5 158 1 PLGF\_MOUSE

27 83.5 13.4 5179 1 MUC2\_HUMAN

28 79.0 12.5 170 1 PLGF\_HUMAN

29 77.5 12.5 3672 1 LML2\_CABEL

30 73.0 11.8 60 1 MT\_CHAAC

31 73.0 11.8 60 1 MT\_PAGB

32 73.0 11.8 60 1 MT\_PARCR

33 11.6 1 1 MT\_DICLAR

34 72 11.6 171 1 LMEL\_HYDAT

35 71.5 11.5 3712 1 LMAD\_DRONE

36 71 11.4 60 1 MT\_OREMO

37 71 11.4 82 1 MT2B\_LYCES

38 71 11.4 846 1 ITBX\_DRONE

39 70 11.4 68 1 MT2\_HORSE

40 70 11.3 68 1 MT3\_PIG

41 70 11.3 60 1 MT\_LIZAU

42 69 11.1 82 1 MT2I\_ORRISA

43 69 11.1 899 1 SUHW\_DRONI

44 69 11.0 60 1 MTB\_ONCHY

## ALIGNMENTS

RESULT 1  
 VEGH\_ORFN7 ID VEGH\_ORFN7 STANDARD; PRT; 148 AA.  
 AC P52585;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE VASCULAR ENDOTHELIAL GROWTH FACTOR HOMOLOG PRECURSOR.  
 GN A2R.  
 RA Lytle D.J., Fraser K.M., Fleming S.B., Mercer A.A., Robinson A.J.;  
 RT Homologs of vascular endothelial growth factor are encoded by the poxvirus (strain NZ7) (CV NZ-7).  
 OS Orf virus (strain NZ7) (CV NZ-7).  
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
 OC Parapoxvirus.  
 OX NCBI\_TaxID=73495;  
 RN [1] J. Virol. 68: 84-92 (1994).  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9407645; PUBMED=8254780;  
 RA Little D.J., Fraser K.M., Fleming S.B., Mercer A.A., Robinson A.J.;  
 RT "Homologs of vascular endothelial growth factor are encoded by the poxvirus (strain NZ7) (CV NZ-7)."  
 RL J. Virol. 68: 84-92 (1994).  
 CC J. FUNCTION: INDUCES ENDOTHELIAL PROLIFERATION.  
 CC J. SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.  
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 CC DR EMBL; S6752; RAB2923.1; -.  
 DR HSSP; P1562; LVPF.  
 DR Interpro; IPR00072; -.  
 DR Pfam; PF00341; PDGF; 1.  
 DR PROSITE; PS00249; PDGF\_1; FALSE\_NEG.  
 DR PROSITE; PS00278; PDGF\_2; 1.  
 DR MITOGEN; Growth factor; Glycoprotein; Signal.  
 FT SIGNAL 1 ? POTENTIAL.  
 FT CHAIN ? VASCULAR ENDOTHELIAL GROWTH FACTOR HOMOLOG.  
 FT DISULFID ? BY SIMILARITY.  
 FT DISULFID 46 88 BY SIMILARITY.  
 FT DISULFID 77 130 BY SIMILARITY.  
 FT DISULFID 81 132 BY SIMILARITY.  
 FT DISULFID 71 71 INTERCHAIN (BY SIMILARITY).  
 FT DISULFID 80 80 INTERCHAIN (BY SIMILARITY).  
 FT CARBOHYD 95 95 N-LINED (GLCNAC -) (POTENTIAL).  
 SQ SEQUENCE 148 AA: 16078 MW: F0E3BA104CC7F8 CRC64;

Query Match 18.4%; Score 114.5; DB 1; Length 148;  
 Best Local Similarity 30.2%; Pred. No. 3.5e-05;  
 Matches 29; Conservative 19; Mismatches 43; Index 5; Gaps 3;  
 Qy 16 CTPRNFVSVIREEEL-KRTDTIFWPQGCLLVKRCGGNCACCLHCNCOCVPSKVKYHEV 74  
 Qyptg99 dicentrarch

RESULT 3

Db 98 CKTRTVIYEPRSQDPTSANFLINPVCVKRCNG---CC---NTSSVKCOPSRV---HH 149



FT	SIGNAL	1	22	RL	Nature 316:748-750(1985).
FT	PROPEP	23	91	RN	[5]
FT	CHAIN	92	226	RP	SEQUENCE FROM N.A.
FT	DISULFID	101	145	RX	MEDLINE=85209623; PubMed=2991848;
FT	DISULFID	134	182	RA	Ratner L., Josephs S.F., Jarrett R., Reitz M.S., Wong-Staal F.;
FT	DISULFID	138	184	RT	"Nucleotide sequence of transforming human C-sis cDNA clones with
FT	DISULFID	128	128	RT	homology to platelet-derived growth factor.";
FT	DISULFID	137	137	RL	Nucleic Acids Res. 13:5007-5018(1985).
FT	CARBONYD	139	139	RN	[6]
FT	VARSPLIC	198	200	RP	SEQUENCE FROM N.A.
FT	VARSPLIC	201	226	RX	MEDLINE=8721119; PubMed=3472769;
FT	CONFFLICT	199	209	RA	Rao C.D., Igarashi H., Pech M.W., Robbins K.C., Aaronson S.A.;
FT	SEQUENCE	218	218	RT	"Oncogenic potential of the human platelet-derived growth factor
FT	CONFFLICT	226	AA:	RT	transcriptional unit.";
FT	SEQUENCE	25719	MW:	RL	Cold Spring Harb. Symp. Quant. Biol. 51:959-966(1986).
FT	SEQUENCE	226	AA:	RN	[7]
Best	Local Similarity	31.4%	Score 105; DB 1; Length 226;	RP	SEQUENCE FROM N.A.
Matches	33;	Conservative	Pred No. 0.00051; Mismatches 32; Indels 26; Gaps 8;	RA	Burgess J., Odell C.;
Qy	16	CTPRNFSVSI-REELKRKDTIF--WPGCLLVLVRGGNCACCLHNCCNCQCVPVKTKYH	72	RL	Submitted (Oct-1996) to the EMBL/GenBank/DBJ databases.
Db	101	CKTRRTVIEIPRSQIDPTSANFLWPPCVEVKRTG--CC--NTSSVVKCOPSR--HH	152	RN	[8]
Qy	73	-----EVLOQLRKTOVGRGLHKSLSLTOALEHHECCDCVCRGST	109	RP	SEQUENCE OF 1-53 FROM N.A.
Db	153	RSVVKVAKVEYVRKKP-----LKEVL-VRLLEHLECTCTANSNS	190	RX	MEDLINE=9711927; PubMed=8988177;
RESULT	6			RA	Simon M.-P., Pedetour F., Sirvent N., Grosgeorge J., Minoletti F.,
ID	PODB_HUMAN	STANDARD:	PRT: 241 AA.	RA	Coindre J.-M., Terrier-Lacombe M.-J., Mandahl N., Kedra D.,
AC	P01127; P78431;			RA	Blin N., Sozzi G., Turc-Carel C., O'Brien K.P., Kedra D.,
DT	21-JUL-1986 (Rel. 01, Created)			RA	Fransson I., Guilbaud C., Dumanski J.P.;
DT	21-JUL-1986 (Rel. 01, Last sequence update)			RT	"Deregulation of the platelet-derived growth factor B-chain gene via
DE	01-OCT-2000 (Rel. 40, Last annotation update)			RT	fusion with collagen gene COL1A1 in dermatofibrosarcoma protuberans
DE	PLATELET-DERIVED GROWTH FACTOR, B CHAIN PRECURSOR (PDGF B-CHAIN)			RT	and giant-cell fibroblastoma.";
DE	(PDGF-2) (C-SIS) (BECAPLERMIN).			RT	Nat. Genet. 15:95-98(1997).
GN	PDGF B OR SIS.			RN	[9]
OS	Homo sapiens (Human); Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo. [1]			RP	SEQUENCE FROM N.A.
OC	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo. [1]			RX	RX
OX	NCBI_TAXID=9606;			RA	Medline:86164981; Published=3456904;
RN	SEQUENCE FROM N.A.			RA	Welch H.A., Sebald W., Schärlie H.U., Hoppe J.;
RP	MEDLINE=84250225; PubMed=6740330;			RT	"The human osteosarcoma cell line U-2 OS expresses a 3.8 kilobase mRNA which codes for the sequence of the PDGF-B chain.";
RX	JOSEPHS S.F., Ratner L., Clarke M.F., Westin E.H., Reitz M.S., Wong-Staal F.;			RT	FEBS Lett. 198:344-348(1986).
RA	"Transforming potential of human c-sis nucleotide sequences encoding platelet-derived growth factor.";			RN	[10]
RA	Science 225:636-639(1984).			RP	SEQUENCE OF 153-200 FROM N.A. AND PARTIAL SEQUENCE.
RA	SEQUENCE FROM N.A.			RX	MEDLINE=84226121; PubMed=6229745;
RA	RHEDLINE=84250225; PubMed=6740330;			RA	Johnson A., Heldin C.H., Westermark B., Deuel T.F., Stroobant P., Waterfield M.D., Gray A., Ulrich A., Scrace G.,
RA	JOSEPHS S.F., Ratner L., Clarke M.F., Westin E.H., Reitz M.S., Wong-Staal F.;			RA	Huang J.S., Seeburg P.H.,
RA	"The c-sis gene encodes a precursor of the B chain of platelet-derived growth factor.";			RA	Stroobant P., Waterfield M.D., Gray A., Ulrich A., Scrace G.,
RA	EMBO J. 3:921-928(1984).			RT	EMBO J. 3:921-928(1984).
RN	SEQUENCE OF 26-241 FROM N.A.			RN	[11]
RN	RHEDLINE=84250225; PubMed=6740330;			RP	SEQUENCE OF 82-110.
RN	JOSEPHS S.F., Ratner L., Clarke M.F., Westin E.H., Reitz M.S., Wong-Staal F.;			RX	MEDLINE=83191379; PubMed=6844921;
RN	"Transforming potential of human c-sis nucleotide sequences encoding platelet-derived growth factor.";			RA	Anton-Ledes H.N., Hunkapiller M.W.;
RN	Science 225:636-639(1984).			RT	"Human platelet-derived growth factor (PDGF): amino-terminal amino acid sequence.";
RN	SEQUENCE FROM N.A.			RT	Science 220:963-965(1983).
RX	MEDLINE=86205961; PubMed=632048;			RN	[12]
RA	RAO C.D., Igarashi H., CHIU I.-M., Robbins K.C., Aaronson S.A.;			RP	SEQUENCE OF 82-112.
RA	"Structure and sequence of the human c-sis/platelet-derived growth factor 2 (SIS/PDG2) transcriptional unit.";			RX	MEDLINE=83244981; PubMed=6306471;
RA	RT			RA	Waterfield M.D., Scraff G.T., Whittle N., Stroobant P., Johnson A.,
RA	RT			RA	Waterson A., Westermark B., Heldin C.H., Huang J.S., Deuel T.F.;
RA	RT			RT	"Platelet-derived growth factor is structurally related to the putative transforming protein p28s of simian sarcoma virus.";
RA	RT			RT	Nature 304:35-39(1983).
RA	RT			RN	[13]
RA	SEQUENCE FROM N.A.			RP	MUTAGENESIS, & IMPORTANCE OF ARG-108 AND ILE-111 FOR RECEPTOR-BINDING.
RA	RA			RX	MEDLINE=92097530; PubMed=1661670;
RA	RT			RA	Clements J.M., Bawden L.J., Bloxidge R.E., Catlin G., Cook A.L.,
RA	RT			RA	Craig S., Drummond A.H., Edwards R.M., Fallon A., Green D.R.,
RA	RT			RA	Heilewell P.G., Kirwin P.M., Navee P.D., Richardson S.J., Brown D.,
RA	RT			RA	Chahwala S.B., Sharpe M., Winslow D.;
RA	RT			RA	"Two PDGF-B chain residues, arginine 27 and isoleucine 30, mediate receptor binding and activation.";
RA	RT			RA	EMBO J. 10:4113-4120(1991).
RA	RT			RN	[14]
RA	"Cultured human endothelial cells express platelet-derived growth factor B chain: cDNA cloning and structural analysis.";			RP	INTERCHAIN DISULFIDE BONDS.





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DR EMBL: M22977; AAA35789\_1; --.  
DR EMBL: M27281; AAA36807\_1; --.  
DR EMBL: M23978; AAA36804\_1; --.  
DR EMBL: M23971; AAA36804\_1; JOINED.  
DR EMBL: M23972; AAA36804\_1; JOINED.  
DR EMBL: M23973; AAA36804\_1; JOINED.  
DR EMBL: M23974; AAA36804\_1; JOINED.  
DR EMBL: M23975; AAA36804\_1; JOINED.  
DR EMBL: M23976; AAA36804\_1; JOINED.  
DR EMBL: M23977; AAA36804\_1; JOINED.  
DR EMBL: X62568; CAR44447\_1; --.  
DR PIR: A34492; A34492.  
DR PIR: A40079; A40079.  
DR PIR: A40080; A40080.  
DR PIR: A40454; A40454.  
DR PIR: B40454; B40454.  
DR PIR: C40454; C40454.  
DR PIR: JO1463; JO1463.  
DR PIR: JO1464; JO1464.  
DR PIR: S11348; S11348.  
DR PDB: 1VCH; 08-APR-98.  
DR PDB: 2VGH; 08-APR-98.  
DR PDB: 1VFP; 08-APR-98.  
DR PDB: 2VFP; 29-JUL-98.  
DR PDB: 1VPP; 23-FEB-99.  
DR PDB: 192240; --.  
DR InterPro: IPR00072; --.  
DR Pfam: PF00341; PDGF; 1.  
DR PROSITE: PS00249; PDGF\_1; 1.  
DR PROSITE: PS00278; PDGF\_2; 1.  
KW MITOGEN; GROWTH FACTOR; GLYCOPROTEIN; Alternative splicing; Signal;  
3D-STRUCTURE.  
FT SIGNAL 1 26 VASCULAR ENDOTHELIAL GROWTH FACTOR.  
FT CHAIN 27 215  
FT DISULFID 52 94  
FT DISULFID 83 128  
FT DISULFID 87 130  
FT DISULFID 77 77  
FT DISULFID 86 86  
FT CARBOHYO 101 101  
FT VARSPLIC 141 141  
FT VARSPLIC 142 165  
FT VARSPLIC 142 209  
SQ SEQUENCE 215 AA: 25173 MW: 789759AD5871FF33 CRC64;

Query Match 16.8%; Score 101.5; DB 1; Length 215;  
Best local Similarity 27.0%; Pred. No. 0.00054; Mismatches 33; Indels 11; Gaps 4;  
Matches 24; Conservative 21; Mismatches 33; Indels 11; Gaps 4;

Qy 16 CTPRNFSVIREL-KRDTDFPGCLVKGRCGNACCLHNGNECCVPSKVKYHEV 74  
Db 52 CHPETLVDIFQSPDETEYIFFPSCVPLMRCG--CC--NDEGLECVPTERSNITM01 106

Qy 75 LQLRPTKGTVGLHSLTDVALEHHEECDC 103  
Db 107 MTKPKHOG----OHIGEMSFLOHNKCBC 130

RESULT 9

PDGA\_RAT ID PDGA\_RAT STANDARD: PRT: 204 AA.  
AC P28376;  
DT 01-DEC-1992 (Rel. 24, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)

DE PLATELET-DERIVED GROWTH FACTOR, A CHAIN PRECURSOR (PDGF A-CHAIN) (PDGF-1).  
DE PDGF A OR RPA1.  
GN Rattus norvegicus (Rat).  
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OC NCBI\_TaxID=10116;  
RN [1] --.  
RP SEQUENCE OF 8-204 FROM N.A.  
RX MEDLINE:93305723; PubMed=8318539;  
RA Herren B., Meyer K.A., Rouge M., Loetscher P., Pech M.;  
RT "Conservation in sequence and affinity of human and rodent PDGF  
RT ligands and receptors";  
RL Biochim. Biophys. Acta 1173:294-302(1993).  
RN [2] --.  
RP SEQUENCE FROM N.A.  
RX MEDLINE:9319115; PubMed=8447423;  
RA Katayose D., Ohe M., Yamachii K., Ogata M., Shirato K., Fujita H.,  
RA ShibaHara S., Takishima T.;  
RT "Increased expression of PDGF A- and B-chain genes in rat lungs with  
hypoxic pulmonary hypertension";  
RT Am. J. Physiol. 264:L100-L106(1993).  
RN [3] --.  
RP SEQUENCE OF 58-196 FROM N.A. (SHORT FORM).  
RC XIA Y., Feng L., Tang W.W., Wilson C.B.;  
RX MEDLINE:93225589; PubMed=8469035;  
RT "Cloning and expression of rat platelet-derived growth factor  
A-chain";  
RT J. Am. Soc. Nephrol. 3:622-622(1992).  
RL Mech. Ageing Dev. 67:79-89(1993).  
CC SEQUENCE OF 58-196 FROM N.A. (SHORT FORM).  
CC STRAIN=FISCHER 344; TISSUE=Smooth muscle;  
CC MEDLINE:93225589; PubMed=8469035;  
CC Scabo P., Weksler D., Whittington E., Weksler B.B.;  
CC "The age-dependent proliferation of rat aortic smooth muscle cells is  
independent of differential splicing of PDGF A-chain mRNA";  
CC independent of differentially splicing of PDGF A-chain mRNA.  
CC Mech. Ageing Dev. 67:79-89(1993).  
CC --. FUNCTION: PLATELET-DERIVED GROWTH FACTOR IS A POTENT MITOGEN FOR  
CC CELLS OF MESENCHYMAL ORIGIN. BINDING OF THIS GROWTH FACTOR TO ITS  
CC AFFINITY RECEPTOR ELICTS A VARIETY OF CELLULAR RESPONSES. IT IS  
CC RELEASED BY PLATELETS UPON WOUNDING AND PLAYS AN IMPORTANT ROLE  
CC IN STIMULATING ADJACENT CELLS TO GROW AND THEREBY HEAL THE WOUND.  
CC --. SUBUNIT: ANTI-PARALLEL DISULFIDE-LINKED DIMER OF NON-IDENTICAL (A  
CC AND B) CHAINS. HOMODIMERS OF A AND B CHAINS ARE IMPLICATED IN  
CC TRANSFORMATION PROCESSES.  
CC --. ALTERNATIVE PRODUCTS: 2 ISOFORMS: A LONG FORM (SHOWN HERE) AND A  
CC SHORT FORM: ARE PRODUCED BY ALTERNATIVE SPlicing. THE LONG FORM  
CC CONTAINS A BASIC INSERT WHICH ACTS AS A CELL RETENTION SIGNAL.  
CC --. DEVELOPMENTAL STAGE: IN KIDNEY EPITHELIAL TISSUES, THE SHORTER  
CC FORM PREDOMINATES IN YOUNG (1 DAY OLD) RATS WHILE THE LONGER FORM  
CC BECOMES MORE PREVALANT DURING AGING. THE LONGER FORM  
CC --. MISCELLANEOUS: A-B AND B-B, AS WELL AS A-B, DIMERS CAN BIND TO THE  
CC --. PDGF RECEPTOR.  
CC --. SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.  
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CC --.  
DR EMBL: L06894; AAB59693\_1; --.  
DR InterPro: IPR00072; --.  
DR InterPro: IPR002400; --.  
DR Pfam: PF00341; PDGF; 1.  
DR PRINTS: PR00438; GFCVSNNOT.  
DR PROSITE: PS00249; PDGF\_1; 1.

RK	PROKSIK; F502J; Rock_2; 1. Growth factor; Platelet; Alternative splicing; Glycoprotein; Mitogen; Signal.	RX	SEQUENCE FROM N.A.
KW	1 20	RA	MEDLINE-88030611; PubMed-36661150;
FT	BY SIMILARITY.	RA	Hoppe J., Schumacher L., Eichner W., Welch H.A.;
PROPEP	21 85	RT	The long 3'-untranslated regions of the PDGF-A and -B mRNAs are only
FT	REMOVED BY PROTEOLYSIS.	RT	distantly related.;
CHAIN	86 204	RT	FEBS Lett. 223:243-246(1987).
FT	SITE 156 162	RN	[5]
FT	DISULFID 96 140	RP	SEQUENCE OF 1-53 FROM N.A.
FT	DISULFID 129 177	RX	MEDLINE-9325628; PubMed-846521;
FT	DISULFID 133 179	RA	Takimoto Y., Li W.Y., Wang T.Y., Tong B.D., Deuel T.F.;
FT	DISULFID 123 123	RT	"Nucleotide sequence of the 5' region of the human platelet-derived
FT	DISULFID 132 132	RT	growth factor A-chain gene.";
FT	DISULFID 134 134	RL	Hiroshima J. Med. Sci. 42:47-52(1993).
FT	DISULFID 194 196	RN	[6]
FT	DISULFID 197 204	RX	ALTERNATIVE SPlicing.
FT	DISULFID 85 111	RA	MEDLINE-8728747; PubMed-3614363;
FT	DISULFID 70 119	RA	Tong B.D., Auer D.E., Jaye M., Kaplow J.M., Ricca G., McConathy E.,
FT	DISULFIDE 204 AA: 23307 MW: FM41374E6F742C CRC64;	RA	Drohan W., Deuel T.F.;
FT	DISULFIDE 151 KVAKVERVKKPKLKEV----QVRLLEHLECAC 179	RT	"cDNA clones reveal differences between human glial and endothelial
FT	DISULFIDE 151 KVAKVERVKKPKLKEV----QVRLLEHLECAC 179	RT	cell platelet-derived growth factor A-chains.";
FT	DISULFIDE 150 KYHEVQLQPLKTVGVRGLHKLTDVALEHHECDC 103	RT	Nature 328:619-621(1987).
FT	DISULFIDE 204 AA: 23307 MW: FM41374E6F742C CRC64;	RN	[7]
FT	DISULFIDE 151 KVAKVERVKKPKLKEV----QVRLLEHLECAC 179	RP	ALTERNATIVE SPlicing.
FT	DISULFIDE 151 KVAKVERVKKPKLKEV----QVRLLEHLECAC 179	RX	MEDLINE-8728748; PubMed-3614364;
FT	DISULFIDE 151 KVAKVERVKKPKLKEV----QVRLLEHLECAC 179	RA	Collins T., Bonthron D.T., Orkin S.H.;
FT	DISULFIDE 151 KVAKVERVKKPKLKEV----QVRLLEHLECAC 179	RT	"Alternative RNA Splicing" affects function of encoded platelet-derived
FT	DISULFIDE 151 KVAKVERVKKPKLKEV----QVRLLEHLECAC 179	RT	growth factor A-chain.;
FT	DISULFIDE 151 KVAKVERVKKPKLKEV----QVRLLEHLECAC 179	RL	Nature 328:621-624(1987).;
FT	DISULFIDE 151 KVAKVERVKKPKLKEV----QVRLLEHLECAC 179	RN	[8]
FT	DISULFIDE 151 KVAKVERVKKPKLKEV----QVRLLEHLECAC 179	RP	INTERCHAIN DISULFIDE BONDS.
FT	DISULFIDE 151 KVAKVERVKKPKLKEV----QVRLLEHLECAC 179	RX	MEDLINE-9228833; PubMed-1317862;
FT	DISULFIDE 151 KVAKVERVKKPKLKEV----QVRLLEHLECAC 179	RA	Andersson M., Oestman A., Baekstroem G., Hellman U.,
FT	DISULFIDE 151 KVAKVERVKKPKLKEV----QVRLLEHLECAC 179	RA	George-Nascimento C., Westermark B., Heldin C.-H.;
FT	DISULFIDE 151 KVAKVERVKKPKLKEV----QVRLLEHLECAC 179	RT	"Assignment of interchain disulfide bonds in platelet-derived growth
FT	DISULFIDE 151 KVAKVERVKKPKLKEV----QVRLLEHLECAC 179	RT	factor (PDGF) and evidence for agonist activity of monomeric PDGF.";
FT	DISULFIDE 151 KVAKVERVKKPKLKEV----QVRLLEHLECAC 179	RL	J. Biol. Chem. 267:11260-11266(1992).
FT	DISULFIDE 151 KVAKVERVKKPKLKEV----QVRLLEHLECAC 179	CC	-- FUNCTION: PLATELET-DERIVED GROWTH FACTOR IS A POTENT MITOGEN FOR
FT	DISULFIDE 151 KVAKVERVKKPKLKEV----QVRLLEHLECAC 179	CC	CELLS OF MESENCHYMAL ORIGIN. BINDING OF THIS GROWTH FACTOR TO ITS
FT	DISULFIDE 151 KVAKVERVKKPKLKEV----QVRLLEHLECAC 179	CC	AFFINITY RECEPTOR ELICTS A VARIETY OF CELLULAR RESPONSES. IT IS
FT	DISULFIDE 151 KVAKVERVKKPKLKEV----QVRLLEHLECAC 179	CC	RELEASED BY PLATELETS UPON WOUNDING AND PLAYS AN IMPORTANT ROLE
FT	DISULFIDE 151 KVAKVERVKKPKLKEV----QVRLLEHLECAC 179	CC	IN STIMULATING ADJACENT CELLS TO GROW AND THEREBY HEAL THE WOUND.
FT	DISULFIDE 151 KVAKVERVKKPKLKEV----QVRLLEHLECAC 179	CC	-- SUBUNIT: ANTIPARALLEL DISULFIDE-LINKED DIMER OF NONIDENTICAL (A
FT	DISULFIDE 151 KVAKVERVKKPKLKEV----QVRLLEHLECAC 179	CC	AND B) CHAINS. HOMODIMERS OF A AND B CHAINS ARE IMPLICATED IN
FT	DISULFIDE 151 KVAKVERVKKPKLKEV----QVRLLEHLECAC 179	CC	TRANSFORMATION PROCESSES.
FT	DISULFIDE 151 KVAKVERVKKPKLKEV----QVRLLEHLECAC 179	CC	-- ALTERNATIVE PRODUCTS: 2 ISOFORMS: A LONG FORM (SHOWN HERE) AND A
FT	DISULFIDE 151 KVAKVERVKKPKLKEV----QVRLLEHLECAC 179	CC	SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPlicing. THE LONG FORM
FT	DISULFIDE 151 KVAKVERVKKPKLKEV----QVRLLEHLECAC 179	CC	CONTAINS A BASIC INSERT WHICH ACTS AS A CELL RETENTION SIGNAL.
FT	DISULFIDE 151 KVAKVERVKKPKLKEV----QVRLLEHLECAC 179	CC	-- MISCELLANEOUS: A-A AND B-B, AS WELL AS A-B, DIMERS CAN BIND TO THE
FT	DISULFIDE 151 KVAKVERVKKPKLKEV----QVRLLEHLECAC 179	CC	PDGF RECEPTOR.
FT	DISULFIDE 151 KVAKVERVKKPKLKEV----QVRLLEHLECAC 179	CC	-- SIMILARITY: BELONGS TO THE PDGF/VEGFR FAMILY OF GROWTH FACTORS.
FT	DISULFIDE 151 KVAKVERVKKPKLKEV----QVRLLEHLECAC 179	CC	-- DATABASE: NAME=R&D Systems' Cytokine source book;
FT	DISULFIDE 151 KVAKVERVKKPKLKEV----QVRLLEHLECAC 179	CC	WWW="http://www.rndsystems.com/cyt_cat/pdgf.html".
FT	DISULFIDE 151 KVAKVERVKKPKLKEV----QVRLLEHLECAC 179	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
FT	DISULFIDE 151 KVAKVERVKKPKLKEV----QVRLLEHLECAC 179	CC	between the Swiss Institute of Bioinformatics and the EMBL outstation. Its
FT	DISULFIDE 151 KVAKVERVKKPKLKEV----QVRLLEHLECAC 179	CC	use by non-profit institutions as long as its content is in no way
FT	DISULFIDE 151 KVAKVERVKKPKLKEV----QVRLLEHLECAC 179	CC	modified and this statement is not removed. Usage by and for commercial
FT	DISULFIDE 151 KVAKVERVKKPKLKEV----QVRLLEHLECAC 179	CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/
FT	DISULFIDE 151 KVAKVERVKKPKLKEV----QVRLLEHLECAC 179	CC	or send an email to license@isb-sib.ch).
FT	DISULFIDE 151 KVAKVERVKKPKLKEV----QVRLLEHLECAC 179	CC	-----
FT	DISULFIDE 151 KVAKVERVKKPKLKEV----QVRLLEHLECAC 179	DR	EMBL: M21571; --; NOT_ANNOTATED_CDS.
FT	DISULFIDE 151 KVAKVERVKKPKLKEV----QVRLLEHLECAC 179	DR	EMBL: X03795; CAA27421; --.
FT	DISULFIDE 151 KVAKVERVKKPKLKEV----QVRLLEHLECAC 179	DR	EMBL: X06374; CAA29677; --.
FT	DISULFIDE 151 KVAKVERVKKPKLKEV----QVRLLEHLECAC 179	DR	EMBL: M020494; AA60045; --.
FT	DISULFIDE 151 KVAKVERVKKPKLKEV----QVRLLEHLECAC 179	DR	EMBL: M20488; AA60045; --.
FT	DISULFIDE 151 KVAKVERVKKPKLKEV----QVRLLEHLECAC 179	DR	EMBL: M020491; AA60045; --.
FT	DISULFIDE 151 KVAKVERVKKPKLKEV----QVRLLEHLECAC 179	DR	EMBL: M20492; AA60045; --.
FT	DISULFIDE 151 KVAKVERVKKPKLKEV----QVRLLEHLECAC 179	DR	EMBL: M20493; AA60045; --.
FT	DISULFIDE 151 KVAKVERVKKPKLKEV----QVRLLEHLECAC 179	DR	EMBL: M19988; AA60046; --.
FT	DISULFIDE 151 KVAKVERVKKPKLKEV----QVRLLEHLECAC 179	DR	EMBL: M21571; AA60046; --.



RESULT 13

OS	Sus scrofa (Pig); Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC	NCBI_TaxID=9823;	NCBI_TaxID=9806;
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.	[1]	SEQUENCE FROM N.A.
OX		RX	SEQUENCE FROM N.A., AND SEQUENCE OF 103-120.
RN		RX	MEDLINE-95143284; PubMed-7841203;
RP		RX	MEDLINE-96178224; PubMed-8617204;
RA	Sharma H.S., Tang Z.H., Gho B.C.H., Verdouw P.D.;	RX	"A novel vascular endothelial growth factor, VEGF-C, is a ligand for the Flt4 (VEGFR-3) and KDR (VEGFR-2) receptor tyrosine kinases.;"
RT	"Nucleotide sequence and expression of the porcine vascular endothelial growth factor";	RX	JOKKOV V., Pajusola K., Kalpainen A., Chilov D., Lahtinen I., Kukk E.,
RL	endothelial growth factor";	RX	Saksela O., Kalkkinen N., Alitalo K.;
RL	Biochim. Biophys. Acta 1260:235-238(1995).	RX	EMBO J. 15:290-298(1996).
CC	-!- FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS, AND ENDOTHELIAL CELL GROWTH. INDUCES ENDOTHELIAL PROLIFERATION AND VASCULAR PERMEABILITY (BY SIMILARITY).	RX	[2]
CC	-!- SUBUNIT: HOMODIMER. DISULFIDE-LINKED (BY SIMILARITY). BUT REMAINS ASSOCIATED TO CELLS OR TO THE EXTRACELLULAR MATRIX UNLESS RELEASED BY HEPARIN (BY SIMILARITY).	RX	ERRATUM.
CC	-!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.	RX	MEDLINE-96203094; PubMed-8612600;
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).	RX	JOKKOV V., Pajusola K., Kalpainen A., Chilov D., Lahtinen I., Kukk E., Saksela O., Kalkkinen N., Alitalo K.;
CC	EMBL: X81380; CA57143.1; -.	RX	EMBO J. 15:1751-1751(1996).
CC	DR HSSP: P15692; 2V0H; InterPro: IPR000072; -.	RX	[3]
CC	DR Pfam: PF00341; PDGF_1.	RX	SEQUENCE FROM N.A.
CC	DR PROSITE: PS00249; PDGF_1; 1.	RX	MEDLINE-96312526; PubMed-8700872;
CC	DR PROSITE: PS00278; PDGF_2; 1.	RX	Lee J., Gray A., Yuan J., Luoh S.-M., Avraham H., Wood W.I.;
CC	DR KW Mitogen; Growth factor; Glycoprotein; Signal; SIGNAL_1; 25; VASCULAR ENDOTHELIAL GROWTH FACTOR.	RX	Burgess P., Giannotti J., Clarkeletta A., Hennessy D., Kovacic S., Fitzgerald M., Scultrato H., Welch N., Neben S., Finnerty H., Zollner R., Wang J., Nickbarg E., Gassaway R., Turner K., Wood C.R.; Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
CC	FT CHAIN 27 190	RX	CC -!- FUNCTION: GROWTH FACTOR ACTIVE IN ANGIOGENESIS, AND ENDOTHELIAL CELL GROWTH.
CC	FT DISULFID 51 93	RX	CC -!- SUBUNIT: HOMODIMER. DISULFIDE-LINKED.
CC	FT DISULFID 82 127	RX	CC -!- PTM: PROBABLY PROTEOLYTICALLY PROCESSED IN THE C-TERMINUS.
CC	FT DISULFID 86 129	RX	CC -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
CC	FT DISULFID 76 76	RX	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).
CC	FT DISULFID 85 85	RX	CC DR EMBL: X94216; CA63907.1; -.
CC	FT CARBOHYD 100 100	RX	CC DR EMBL: U3142; AAB85214.1; -.
CC	SEQUENCE 190 AA; 22368 MW; 04D40B8D7913047F CRC64;	RX	CC DR EMBL: U58111; AAB02909.1; -.
CC		RX	CC DR HSSP: P15692; 1VPF; MIM: 601528; -.
CC		RX	CC DR InterPro: IPR000072; -.
CC		RX	CC DR Pfam: PF00341; PDGF_1.
CC		RX	CC DR PRINTS: PR00438; GFCYSKNOT.
CC		RX	CC DR PROSITE: PS00249; PDGF_1; 1.
CC		RX	CC DR PROSITE: PS00278; PDGF_2; 1.
CC		RX	CC KW Mitogen; Growth factor; Glycoprotein; Signal; Repeat.
CC		RX	CC FT SIGNAL_1; ? 102 POTENTIAL.
CC		RX	CC FT PROPEP ? 102 POTENTIAL.
CC		RX	CC FT CHAIN 103 419 VASCULAR ENDOTHELIAL GROWTH FACTOR C.
CC		RX	CC FT DOMAIN 275 365 4 X 24 AA TANDEM REPEATS.
CC		RX	CC FT REPEAT 275 298 1.
CC		RX	CC FT REPEAT 299 322 2.
CC		RX	CC FT REPEAT 323 346 3.
CC		RX	CC FT REPEAT 347 365 4 (PARTIAL).
CC		RX	CC FT CARBOHYD 175 205 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC		RX	CC FT CARBOHYD 205 240 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC		RX	CC DE VASCULAR ENDOTHELIAL GROWTH FACTOR C PRECURSOR (VEGF-C) (VASCULAR ENDOTHELIAL GROWTH FACTOR RELATED PROTEIN) (VRP) (FLT4 LIGAND) (FLT4-VEGFR).
OS	Homo sapiens (Human).	RX	OS -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	RX	OS -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
OS	Best Local Similarity 16.5%; Score 102.5; DB 1; Length 419; Pred. No. 0.0017;	RX	OS -!- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.

Matches 31; Conservative 15; Mismatches 43; Indels 21; Gaps 6;  
Qy 4 LNLITEEVLYSCTPRNFSVIRREL-KRDTIWPGLVKGNNCACCLHNNECOC 62  
Db 119 LKSTDNEWRKTOCPRECIDVGKEFGVATNTFFKPPCVSYRGG--CC-NSEGLOC 173  
Qy 63 V---PSKVKKYHV---QLRPPTGVRGLHKSLLDVALEHHEDDCYCR 106  
Db 174 MNTTSYLSKTLFEITVPLSQGPKP-----VTISFANHTSCKRCMSK 214

Search completed: July 3, 2001, 10:33:06  
Job time: 206 sec

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GenCore version 4.5

W protein - protein search, using sw model

un on: July 3, 2001, 10:27:25 ; Search time 18.61 Seconds  
(without alignments)

database : US-09-541-752-2\_COPY\_235-345

title: 621 VWDNLNLTEEVRLYSPTRN.....DVALEHHEECDCVCRSTGG 111

score: 454.346 Million cell updates/sec

sequence: BLOSUM62

Gapop 10.0 , Gapext 0.5

core table: 219241 seqs, 76174552 residues

total number of hits satisfying chosen parameters: 219241

minimum DB seq length: 0

maximum DB seq length: 200000000

post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

PIR\_68:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result	Query	Length	DB	ID	Description	
1	114.5	18.4	148	2	D49530	
2	108.4	16.6	2	JN0248	16K vascular endothelial growth factor homolog A2R - Orf virus	
3	108	17.4	198	2	JS0735	C;Species: Orf virus
4	105	16.9	200	2	151551	C;Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999
5	105	16.9	215	2	S08220	C;Accession: D49530
6	105	16.9	226	2	I51550	R;Lyttle, D.J.; Fraser, K.M.; Fleming, S.B.; Mercer, A.A.; Robinson, A.J.
7	105	16.9	241	1	PPFHUG2	J; Virol. 68, 84-92, 1994
8	105	16.9	245	1	TVCTSS	A;Title: Homologs of vascular endothelial growth factor are encoded by the poxvirus
9	104.5	16.8	232	2	A41551	A;Reference number: A49530, MUID:94075465
10	104	16.7	196	2	B28964	A;Contents: NZ7
11	104	16.7	197	2	S25096	A;Accession: D49530
12	104	16.7	211	1	PPFHUG1	A;Status: preliminary
13	104	16.7	226	1	TVKVSS	A;Molecule type: DNA
14	102.5	16.5	133	2	B49530	A;Residues: 1-148 <LYT>
15	102.5	16.5	190	2	S52130	A;Cross-references: GB:567522; NID:9456900; PIDN:AA829223.1; PID:9456902
16	102.5	16.5	196	2	A37359	A;Note: sequence extracted from NCBI backbone (NCBIn:141422, NCBIp:141426)
17	102.5	16.5	196	2	A48851	
18	102.5	16.5	419	2	S69207	
19	101.5	16.3	120	1	A33787	
20	101.5	16.3	146	2	S57956	
21	101.5	16.3	190	2	B40080	
22	97	15.6	188	2	JC4680	
23	97	15.6	207	2	JC4679	
24	96.5	15.5	190	2	A35987	
25	95.5	15.4	190	2	B44881	
26	95.5	15.4	214	2	A44881	
27	94	15.1	225	2	S25097	
28	94	15.1	241	1	PFMSG2	
29	88	14.2	271	2	A25669	

RESULT 1

Query Match 18.4%; Score 114.5; DB 2; Length 148;

Best Local Similarity 30.2%; Pred. No. 0.00028; Mismatches 43; Indels 5; Gaps 3;

Matches 29; Conservative 19;

Qy 16 CTPRNFSVSVREEL-KRTDTIFWPGCLVKRQGGNCACCLHNCNECCOPSKVTKVHEV 74

Db 46 CKPRDVTYVGLGEYPESTNLQVNPRCVTKVKGSG...CCNGDQICITAVETRNTTVVSV 102

Qy 75 IQLRPKTGVV-GLHKSTTDVALEHHEECDCVCRGST 109

Db 103 TVGSSSSGGTNSGVSTNQCRISVTEHTKCDCIGRTT 138

RESULT 2

Query Match 18.4%; Score 114.5; DB 2; Length 148;

Best Local Similarity 30.2%; Pred. No. 0.00028; Mismatches 43; Indels 5; Gaps 3;

Matches 29; Conservative 19;

Qy 16 CTPRNFSVSVREEL-KRTDTIFWPGCLVKRQGGNCACCLHNCNECCOPSKVTKVHEV 74

Db 46 CKPRDVTYVGLGEYPESTNLQVNPRCVTKVKGSG...CCNGDQICITAVETRNTTVVSV 102

Qy 75 IQLRPKTGVV-GLHKSTTDVALEHHEECDCVCRGST 109

Db 103 TVGSSSSGGTNSGVSTNQCRISVTEHTKCDCIGRTT 138

Qy 16 CTPRNFSVSVREEL-KRTDTIFWPGCLVKRQGGNCACCLHNCNECCOPSKVTKVHEV 74

Db 46 CKPRDVTYVGLGEYPESTNLQVNPRCVTKVKGSG...CCNGDQICITAVETRNTTVVSV 102

Qy 75 IQLRPKTGVV-GLHKSTTDVALEHHEECDCVCRGST 109

Db 103 TVGSSSSGGTNSGVSTNQCRISVTEHTKCDCIGRTT 138

Qy 16 CTPRNFSVSVREEL-KRTDTIFWPGCLVKRQGGNCACCLHNCNECCOPSKVTKVHEV 74

Db 46 CKPRDVTYVGLGEYPESTNLQVNPRCVTKVKGSG...CCNGDQICITAVETRNTTVVSV 102

Qy 75 IQLRPKTGVV-GLHKSTTDVALEHHEECDCVCRGST 109

Db 103 TVGSSSSGGTNSGVSTNQCRISVTEHTKCDCIGRTT 138

Qy 16 CTPRNFSVSVREEL-KRTDTIFWPGCLVKRQGGNCACCLHNCNECCOPSKVTKVHEV 74

Db 46 CKPRDVTYVGLGEYPESTNLQVNPRCVTKVKGSG...CCNGDQICITAVETRNTTVVSV 102

Qy 75 IQLRPKTGVV-GLHKSTTDVALEHHEECDCVCRGST 109

Db 103 TVGSSSSGGTNSGVSTNQCRISVTEHTKCDCIGRTT 138

Qy 16 CTPRNFSVSVREEL-KRTDTIFWPGCLVKRQGGNCACCLHNCNECCOPSKVTKVHEV 74

Db 46 CKPRDVTYVGLGEYPESTNLQVNPRCVTKVKGSG...CCNGDQICITAVETRNTTVVSV 102

Qy 75 IQLRPKTGVV-GLHKSTTDVALEHHEECDCVCRGST 109

Db 103 TVGSSSSGGTNSGVSTNQCRISVTEHTKCDCIGRTT 138

Qy 16 CTPRNFSVSVREEL-KRTDTIFWPGCLVKRQGGNCACCLHNCNECCOPSKVTKVHEV 74

Db 46 CKPRDVTYVGLGEYPESTNLQVNPRCVTKVKGSG...CCNGDQICITAVETRNTTVVSV 102

Qy 75 IQLRPKTGVV-GLHKSTTDVALEHHEECDCVCRGST 109

Db 103 TVGSSSSGGTNSGVSTNQCRISVTEHTKCDCIGRTT 138

Qy 16 CTPRNFSVSVREEL-KRTDTIFWPGCLVKRQGGNCACCLHNCNECCOPSKVTKVHEV 74

Db 46 CKPRDVTYVGLGEYPESTNLQVNPRCVTKVKGSG...CCNGDQICITAVETRNTTVVSV 102

Qy 75 IQLRPKTGVV-GLHKSTTDVALEHHEECDCVCRGST 109

Db 103 TVGSSSSGGTNSGVSTNQCRISVTEHTKCDCIGRTT 138

Qy 16 CTPRNFSVSVREEL-KRTDTIFWPGCLVKRQGGNCACCLHNCNECCOPSKVTKVHEV 74

Db 46 CKPRDVTYVGLGEYPESTNLQVNPRCVTKVKGSG...CCNGDQICITAVETRNTTVVSV 102

Qy 75 IQLRPKTGVV-GLHKSTTDVALEHHEECDCVCRGST 109

Db 103 TVGSSSSGGTNSGVSTNQCRISVTEHTKCDCIGRTT 138

Qy 16 CTPRNFSVSVREEL-KRTDTIFWPGCLVKRQGGNCACCLHNCNECCOPSKVTKVHEV 74

Db 46 CKPRDVTYVGLGEYPESTNLQVNPRCVTKVKGSG...CCNGDQICITAVETRNTTVVSV 102

Qy 75 IQLRPKTGVV-GLHKSTTDVALEHHEECDCVCRGST 109

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Qy 16 CTPRNFSVSVREEL-KRTDTIFWPGCLVKRQGGNCACCLHNCNECCOPSKVTKVHEV 74

Db 46 CKPRDVTYVGLGEYPESTNLQVNPRCVTKVKGSG...CCNGDQICITAVETRNTTVVSV 102

Qy 75 IQLRPKTGVV-GLHKSTTDVALEHHEECDCVCRGST 109

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Qy 16 CTPRNFSVSVREEL-KRTDTIFWPGCLVKRQGGNCACCLHNCNECCOPSKVTKVHEV 74

Db 46 CKPRDVTYVGLGEYPESTNLQVNPRCVTKVKGSG...CCNGDQICITAVETRNTTVVSV 102

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Qy 16 CTPRNFSVSVREEL-KRTDTIFWPGCLVKRQGGNCACCLHNCNECCOPSKVTKVHEV 74

Db 46 CKPRDVTYVGLGEYPESTNLQVNPRCVTKVKGSG...CCNGDQICITAVETRNTTVVSV 102

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Qy 16 CTPRNFSVSVREEL-KRTDTIFWPGCLVKRQGGNCACCLHNCNECCOPSKVTKVHEV 74

Db 46 CKPRDVTYVGLGEYPESTNLQVNPRCVTKVKGSG...CCNGDQICITAVETRNTTVVSV 102

Qy 75 IQLRPKTGVV-GLHKSTTDVALEHHEECDCVCRGST 109

Db 103 TVGSSSSGGTNSGVSTNQCRISVTEHTKCDCIGRTT 138

Qy 16 CTPRNFSVSVREEL-KRTDTIFWPGCLVKRQGGNCACCLHNCNECCOPSKVTKVHEV 74

Db 46 CKPRDVTYVGLGEYPESTNLQVNPRCVTKVKGSG...CCNGDQICITAVETRNTTVVSV 102

Qy 75 IQLRPKTGVV-GLHKSTTDVALEHHEECDCVCRGST 109

Db 103 TVGSSSSGGTNSGVSTNQCRISVTEHTKCDCIGRTT 138

Qy 16 CTPRNFSVSVREEL-KRTDTIFWPGCLVKRQGGNCACCLHNCNECCOPSKVTKVHEV 74

Db 46 CKPRDVTYVGLGEYPESTNLQVNPRCVTKVKGSG...CCNGDQICITAVETRNTTVVSV 102

Qy 75 IQLRPKTGVV-GLHKSTTDVALEHHEECDCVCRGST 109

Db 103 TVGSSSSGGTNSGVSTNQCRISVTEHTKCDCIGRTT 138

Qy 16 CTPRNFSVSVREEL-KRTDTIFWPGCLVKRQGGNCACCLHNCNECCOPSKVTKVHEV 74

Db 46 CKPRDVTYVGLGEYPESTNLQVNPRCVTKVKGSG...CCNGDQICITAVETRNTTVVSV 102

Qy 75 IQLRPKTGVV-GLHKSTTDVALEHHEECDCVCRGST 109

Db 103 TVGSSSSGGTNSGVSTNQCRISVTEHTKCDCIGRTT 138

Qy 16 CTPRNFSVSVREEL-KRTDTIFWPGCLVKRQGGNCACCLHNCNECCOPSKVTKVHEV 74

Db 46 CKPRDVTYVGLGEYPESTNLQVNPRCVTKVKGSG...CCNGDQICITAVETRNTTVVSV 102

Qy 75 IQLRPKTGVV-GLHKSTTDVALEHHEECDCVCRGST 109

Db 103 TVGSSSSGGTNSGVSTNQCRISVTEHTKCDCIGRTT 138

Qy 16 CTPRNFSVSVREEL-KRTDTIFWPGCLVKRQGGNCACCLHNCNECCOPSKVTKVHEV 74

Db 46 CKPRDVTYVGLGEYPESTNLQVNPRCVTKVKGSG...CCNGDQICITAVETRNTTVVSV 102

Qy 75 IQLRPKTGVV-GLHKSTTDVALEHHEECDCVCRGST 109

Db 103 TVGSSSSGGTNSGVSTNQCRISVTEHTKCDCIGRTT 138

Qy 16 CTPRNFSVSVREEL-KRTDTIFWPGCLVKRQGGNCACCLHNCNECCOPSKVTKVHEV 74

Db 46 CKPRDVTYVGLGEYPESTNLQVNPRCVTKVKGSG...CCNGDQICITAVETRNTTVVSV 102

Qy 75 IQLRPKTGVV-GLHKSTTDVALEHHEECDCVCRGST 109

Db 103 TVGSSSSGGTNSGVSTNQCRISVTEHTKCDCIGRTT 138

Qy 16 CTPRNFSVSVREEL-KRTDTIFWPGCLVKRQGGNCACCLHNCNECCOPSKVTKVHEV 74

Db 46 CKPRDVTYVGLGEYPESTNLQVNPRCVTKVKGSG...CCNGDQICITAVETRNTTVVSV 102

Qy 75 IQLRPKTGVV-GLHKSTTDVALEHHEECDCVCRGST 109

Db 103 TVGSSSSGGTNSGVSTNQCRISVTEHTKCDCIGRTT 138

Qy 16 CTPRNFSVSVREEL-KRTDTIFWPGCLVKRQGGNCACCLHNCNECCOPSKVTKVHEV 74

Db 46 CKPRDVTYVGLGEYPESTNLQVNPRCVTKVKGSG...CCNGDQICITAVETRNTTVVSV 102

Qy 75 IQLRPKTGVV-GLHKSTTDVALEHHEECDCVCRGST 109

Db 103 TVGSSSSGGTNSGVSTNQCRISVTEHTKCDCIGRTT 138

Qy 16 CTPRNFSVSVREEL-KRTDTIFWPGCLVKRQGGNCACCLHNCNECCOPSKVTKVHEV 74

Db 46 CKPRDVTYVGLGEYPESTNLQVNPRCVTKVKGSG...CCNGDQICITAVETRNTTVVSV 102

Qy 75 IQLRPKTGVV-GLHKSTTDVALEHHEECDCVCRGST 109

Db 103 TVGSSSSGGTNSGVSTNQCRISVTEHTKCDCIGRTT 138

Qy 16 CTPRNFSVSVREEL-KRTDTIFWPGCLVKRQGGNCACCLHNCNECCOPSKVTKVHEV 74

Db 46 CKPRDVTYVGLGEYPESTNLQVNPRCVTKVKGSG...CCNGDQICITAVETRNTTVVSV 102

Qy 75 IQLRPKTGVV-GLHKSTTDVALEHHEECDCVCRGST 109

Db 103 TVGSSSSGGTNSGVSTNQCRISVTEHTKCDCIGRTT 138

Qy 16 CTPRNFSVSVREEL-KRTDTIFWPGCLVKRQGGNCACCLHNCNECCOPSKVTKVHEV 74

Db 46 CKPRDVTYVGLGEYPESTNLQVNPRCVTKVKGSG...CCNGDQICITAVETRNTTVVSV 102

Qy 75 IQLRPKTGVV-GLHKSTTDVALEHHEECDCVCRGST 109

Db 103 TVGSSSSGGTNSGVSTNQCRISVTEHTKCDCIGRTT 138

Qy 16 CTPRNFSVSVREEL-KRTDTIFWPGCLVKRQGGNCACCLHNCNECCOPSKVTKVHEV 74

Db 46 CKPRDVTYVGLGEYPESTNLQVNPRCVTKVKGSG...CCNGDQICITAVETRNTTVVSV 102

Qy 75 IQLRPKTGVV-GLHKSTTDVALEHHEECDCVCRGST 109

Db 103 TVGSSSSGGTNSGVSTNQCRISVTEHTKCDCIGRTT 138

Qy 16 CTPRNFSVSVREEL-KRTDTIFWPGCLVKRQGGNCACCLHNCNECCOPSKVTKVHEV 74

Db 46 CKPRDVTYVGLGEYPESTNLQVNPRCVTKVKGSG...CCNGDQICITAVETRNTTVVSV 102

Qy 75 IQLRPKTGVV-GLHKSTTDVALEHHEECDCVCRGST 109

Db 103 TVGSSSSGGTNSGVSTNQCRISVTEHTKCDCIGRTT 138

Qy 16 CTPRNFSVSVREEL-KRTDTIFWPGCLVKRQGGNCACCLHNCNECCOPSKVTKVHEV 74

Db 46 CKPRDVTYVGLGEYPESTNLQVNPRCVTKVKGSG...CCNGDQICITAVETRNTTVVSV 102

Qy 75 IQLRPKTGVV-GLHKSTTDVALEHHEECDCVCRGST 109

Db 103 TVGSSSSGGTNSGVSTNQCRISVTEHTKCDCIGRTT 138

Qy 16 CTPRNFSVSVREEL-KRTDTIFWPGCLVKRQGGNCACCLHNCNECCOPSKVTKVHEV 74

Db 46 CKPRDVTYVGLGEYPESTNLQVNPRCVTKVKGSG...CCNGDQICITAVETRNTTVVSV 102

Qy 75 IQLRPKTGVV-GLHKSTTDVALEHHEECDCVCRGST 109

Db 103 TVGSSSSGGTNSGVSTNQCRISVTEHTKCDCIGRTT 138

Qy 16 CTPRNFSVSVREEL-KRTDTIFWPGCLVKRQGGNCACCLHNCNECCOPSKVTKVHEV 74

Db 46 CKPRDVTYVGLGEYPESTNLQVNPRCVTKVKGSG...CCNGDQICITAVETRNTTVVSV 102

Qy 75 IQLRPKTGVV-GLHKSTTDVALEHHEECDCVCRGST 109

Db 103 TVGSSSSGGTNSGVSTNQCRISVTEHTKCDCIGRTT 138

Qy 16 CTPRNFSVSVREEL-KRTDTIFWPGCLVKRQGGNCACCLHNCNECCOPSKVTKVHEV 74

Db 46 CKPRDVTYVGLGEYPESTNLQVNPRCVTKVKGSG...CCNGDQICITAVETRNTTVVSV 102

Qy 75 IQLRPKTGVV-GLHKSTTDVALEHHEECDCVCRGST 109

Db 103 TVGSSSSGGTNSGVSTNQCRISVTEHTKCDCIGRTT 138

Qy 16 CTPRNFSVSVREEL-KRTDTIFWPGCLVKRQGGNCACCLHNCNECCOPSKVTKVHEV 74

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Qy 75 IQLRPKTGVV-GLHKSTTDVALEHHEECDCVCRGST 109

Db 103 TVGSSSSGGTNSGVSTNQCRISVTEHTKCDCIGRTT 138

Qy 16 CTPRNFSVSVREEL-KRTDTIFWPGCLVKRQGGNCACCLHNCNECCOPSKVTKVHEV 74

Db 46 CKPRDVTYVGLGEYPESTNLQVNPRCVTKVKGSG...CCNGDQICITAVETRNTTVVSV 102

Qy 75 IQLRPKTGVV-GLHKSTTDVALEHHEECDCVCRGST 109

Db 103 TVGSSSSGGTNSGVSTNQCRISVTEHTKCDCIGRTT 138

Qy 16 CTPRNFSVSVREEL-KRTDTIFWPGCLVKRQGGNCACCLHNCNECCOPSKVTKVHEV 74

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Qy 75 IQLRPKTGVV-GLHKSTTDVALEHHEECDCVCRGST 109

Db 103 TVGSSSSGGTNSGVSTNQCRISVTEHTKCDCIGRTT 138

Qy 16 CTPRNFSVSVREEL-KRTDTIFWPGCLVKRQGGNCACCLHNCNECCOPSKVTKVHEV 74

Db 46 CKPRDVTYVGLGEYPESTNLQVNPRCVTKVKGSG...CCNGDQICITAVETRNTTVVSV 102

Qy 75 IQLRPKTGVV-GLHKSTTDVALEHHEECDCVCRGST 109

Db 103 TVGSSSSGGTNSGVSTNQCRISVTEHTKCDCIGRTT 138

Qy 16 CTPRNFSVSVREEL-KRTDTIFWPGCLVKRQGGNCACCLHNCNECCOPSKVTKVHEV 74

Db 46 CKPRDVTYVGLGEYPESTNLQVNPRCVTKVKGSG...CCNGDQICITAVETRNTTVVSV 102

Qy 75 IQLRPKTGVV-GLHKSTTDVALEHHEECDCVCRGST 109

Db 103 TVGSSSSGGTNSGVSTNQCRISVTEHTKCDCIGRTT 138

Qy 16 CTPRNFSVSVREEL-KRTDTIFWPGCLVKRQGGNCACCLHNCNECCOPSKVTKVHEV 74

Db 46 CKPRDVTYVGLGEYPESTNLQVNPRCVTKVKGSG...CCNGDQICITAVETRNTTVVSV 102

Qy 75 IQLRPKTGVV-GLHKSTTDVALEHHEECDCVCRGST 109

Db 103 TVGSSSSGGTNSGVSTNQCRISVTEHTKCDCIGRTT 138

Qy 16 CTPRNFSVSVREEL-KRTDTIFWPGCLVKRQGGNCACCLHNCNECCOPSKVTKVHEV 74

Db 46 CKPRDVTYVGLGEYPESTNLQVNPRCVTKVKGSG...CCNGDQICITAVETRNTTVVSV 102

Qy 75 IQLRPKTGVV-GLHKSTTDVALEHHEECDCVCRGST 109

Db 103 TVGSSSSGGTNSGVSTNQCRISVTEHTKCDCIGRTT 138

Qy 16 CTPRNFSVSVREEL-KRTDTIFWPGCLVKRQGGNCACCLHNCNECCOPSKVTKVHEV 74

Db 46 CKPRDVTYVGLGEYPESTNLQVNPRCVTKVKGSG...CCNGDQICITAVETRNTTVVSV 102

Qy 75 IQLRPKTGVV-GLHKSTTDVALEHHEECDCVCRGST 109

Db 103 TVGSSSSGGTNSGVSTNQCRISVTEHTKCDCIGRTT 138

Qy 16 CTPRNFSVSVREEL-KRTDTIFWPGCLVKRQGGNCACCLHNCNECCOPSKVTKVHEV 74

Db 46 CKPRDVTYVGLGEYPESTNLQVNPRCVTKVKGSG...CCNGDQICITAVETRNTTVVSV 102

Qy 75 IQLRPKTGVV-GLHKSTTDVALEHHEECDCVCRGST 109

Db 103 TVGSSSSGGTNSGVSTNQCRISVTEHTKCDCIGRTT 138

Qy 16 CTPRNFSVSVREEL-KRTDTIFWPGCLVKRQGGNCACCLHNCNECCOPSKVTKVHEV 74

Db 46 CKPRDVTYVGLGEYPESTNLQVNPRCVTKVKGSG...CCNGDQICITAVETRNTTVVSV 102

Qy 75 IQLRPKTGVV-GLHKSTTDVALEHHEECDCVCRGST 109

Db 103 TVGSSSSGGTNSGVSTNQCRISVTEHTKCDCIGRTT 138

Qy 16 CTPRNFSVSVREEL-KRTDTIFWPGCLVKRQGGNCACCLHNCNECCOPSKVTKVHEV 74

Db 46 CKPRDVTYVGLGEYPESTNLQVNPRCVTKVKGSG...CCNGDQICITAVETRNTTVVSV 102

Qy 75 IQLRPKTGVV-GLHKSTTDVALEHHEECDCVCRGST 109

Db 103 TVGSSSSGGTNSGVSTNQCRISVTEHTKCDCIGRTT 138

Qy 16 CTPRNFSVSVREEL-KRTDTIFWPGCLVKRQGGNCACCLHNCNECCOPSKVTKVHEV 74

Db 46 CKPRDVTYVGLGEYPESTNLQVNPRCVTKVKGSG...CCNGDQICITAVETRNTTVVSV 102

Qy 75 IQLRPKTGVV-GLHKSTTDVALEHHEECDCVCRGST 109

Db 103 TVGSSSSGGTNSGVSTNQCRISVTEHTKCDCIGRTT 138

Qy 16 CTPRNFSVSVREEL-KRTDTIFWPGCLVKRQGGNCACCLHNCNECCOPSKVTKVHEV 74

Db 46 CKPRDVTYVGLGEYPESTNLQVNPRCVTKVKGSG...CCNGDQICITAVETRNTTVVSV 102

Qy 75 IQLRPKTGVV-GLHKSTTDVALEHHEECDCVCRGST 109

Db 103 TVGSSSSGGTNSGVSTNQCRISVTEHTKCDCIGRTT 138

Qy 16 CTPRNFSVSVREEL-KRTDTIFWPGCLVKRQGGNCACCLHNCNECCOPSKVTKVHEV 74

Db 46 CKPRDVTYVGLGEYPESTNLQVNPRCVTKVKGSG...CCNGDQICITAVETRNTTVVSV 102

Qy 75 IQLRPKTGVV-GLHKSTTDVALEHHEECDCVCRGST 109

Db 103 TVGSSSSGGTNSGVSTNQCRISVTEHTKCDCIGRTT 138

Qy 16 CTPRNFSVSVREEL-KRTDTIFWPGCLVKRQGGNCACCLHNCNECCOPSKVTKVHEV 74

Db 46 CKPRDVTYVGLGEYPESTNLQVNPRCVTKVKGSG...CCNGDQICITAVETRNTTVVSV 102

Qy 75 IQLRPKTGVV-GLHKSTTDVALEHHEECDCVCRGST 109

Db 103 TVGSSSSGGTNSGVSTNQCRISVTEHTKCDCIGRTT 138

Qy 16 CTPRNFSVSVREEL-KRTDTIFWPGCLVKRQGGNCACCLHNCNECCOPSKVTKVHEV 74

Db 46 CKPRDVTYVGLGEYPESTNLQVNPRCVTKVKGSG...CCNGDQICITAVETRNTTVVSV 102

Qy 75 IQLRPKTGVV-GLHKSTTDVALEHHEECDCVCRGST 109

Db 103 TVGSSSSGGTNSGVSTNQCRISVTEHTKCDCIGRTT 138

Qy 16 CTPRNFSVSVREEL-KRTDTIFWPGCLVKRQGGNCACCLHNCNECCOPSKVTKVHEV 74

Db 46 CKPRDVTYVGLGEYPESTNLQVNPRCVTKVKGSG...CCNGDQICITAVETRNTTVVSV 102

Qy 75 IQLRPKTGVV-GLHKSTTDVALEHHEECDCVCRGST 109

Db 103 TVGSSSSGGTNSGVSTNQCRISVTEHTKCDCIGRTT 138

Qy 16 CTPRNFSVSVREEL-KRTDTIFWPGCLVKRQGGNCACCLHNCNECCOPSKVTKVHEV 74

Db 46 CKPRDVTYVGLGEYPESTNLQVNPRCVTKVKGSG...CCNGDQICITAVETRNTTVVSV 102

Qy 75 IQLRPKTGVV-GLHKSTTDVALEHHEECDCVCRGST 109

Db 103 TVGSSSSGGTNSGVSTNQCRISVTEHTKCDCIGRTT 138

Qy 16 CTPRNFSVSVREEL-KRTDTIFWPGCLVKRQGGNCACCLHNCNECCOPSKVTKVHEV 74

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Qy 75 IQLRPKTGVV-GLHKSTTDVALEHHEECDCVCRGST 109

Db 103 TVGSSSSGGTNSGVSTNQCRISVTEHTKCDCIGRTT 138

Qy 16 CTPRNFSVSVREEL-KRTDTIFWPGCLVKRQGGNCACCLHNCNECCOPSKVTKVHEV 74

Db 46 CKPRDVTYVGLGEYPESTNLQVNPRCVTKVKGSG...CCNGDQICITAVETRNTTVVSV 102

Qy 75 IQLRPKTGVV-GLHKSTTDVALEHHEECDCVCRGST 109

Db 103 TVGSSSSGGTNSGVSTNQCRISVTEHTKCDCIGRTT 138

Qy 16 CTPRNFSVSVREEL-KRTDTIFWPGCLVKRQGGNCACCLHNCNECCOPSKVTKVHEV 74

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Qy 75 IQLRPKTGVV-GLHKSTTDVALEHHEECDCVCRGST 109

Db 103 TVGSSSSGGTNSGVSTNQCRISVTEHTKCDCIGRTT 138

Qy 16 CTPRNFSVSVREEL-KRTDTIFWPGCLVKRQGGNCACCLHNCNECCOPSKVTKVHEV 74

Db 46 CKPRDVTYVGLGEYPESTNLQVNPRCVTKVKGSG...CCNGDQICITAVETRNTTVVSV 102

Qy 75 IQLRPKTGVV-GLHKSTTDVALEHHEECDCVCRGST 109

Db 103 TVGSSSSGGTNSGVSTNQCRISVTEHTKCDCIGRTT 138

Qy 16 CTPRNFSVSVREEL-KRTDTIFWPGCLVKRQGGNCACCLHNCNECCOPSKVTKVHEV 74

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Qy 75 IQLRPKTGVV-GLHKSTTDVALEHHEECDCVCRGST 109

Db 103 TVGSSSSGGTNSGVSTNQCRISVTEHTKCDCIGRTT 138

Qy 16 CTPRNFSVSVREEL-KRTDTIFWPGCLVKRQGGNCACCLHNCNECCOPSKVTKVHEV 74

Db 46 CKPRDVTYVGLGEYPESTNLQVNPRCVTKVKGSG...CCNGDQICITAVETRNTTVVSV 102

Qy 75 IQLRPKTGVV-GLHKSTTDVALEHHEECDCVCRGST 109

Db 103 TVGSSSSGGTNSGVSTNQCRISVTEHTKCDCIGRTT 138

Qy 16 CTPRNFSVSVREEL-KRTDTIFWPGCLVKRQGGNCACCLHNCNECCOPSKVTKVHEV 74

Db 46 CKPRDVTYVGLGEYPESTNLQVNPRCVTKVKGSG...CCNGDQICITAVETRNTTVVSV 102

Qy 75 IQLRPKTGVV-GLHKSTTDVALEHHEECDCVCRGST 109

Db 103 TVGSSSSGGTNSGVSTNQCRISVTEHTKCDCIGRTT 138

Qy 16 CTPRNFSVSVREEL-KRTDTIFWPGCLVKRQGGNCACCLHNCNECCOPSKVTKVHEV 74

Db 46 CKPRDVTYVGLGEYPESTNLQVNPRCVTKVKGSG...CCNGDQICITAVETRNTTVVSV 102

Qy 75 IQLRPKTGVV-GLHKSTTDVALEHHEECDCVCRGST 109

Db 103 TVGSSSSGGTNSGVSTNQCRISVTEHTKCDCIGRTT 138

Qy 16 CTPRNFSVSVREEL-KRTDTIFWPGCLVKRQGGNCACCLHNCNECCOPSKVTKVHEV 74

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Qy 75 IQLRPKTGVV-GLHKSTTDVALEHHEECDCVCRGST 109

Db 103 TVGSSSSGGTNSGVSTNQCRISVTEHTKCDCIGRTT 138

Qy 16 CTPRNFSVSVREEL-KRTDTIFWPGCLVKRQGGNCACCLHNCNECCOPSKVTKVHEV 74

Db 46 CKPRDVTYVGLGEYPESTNLQVNPRCVTKVKGSG...CCNGDQICITAVETRNTTVVSV 102

Qy 75 IQLRPKTGVV-GLHKSTTDVALEHHEECDCVCRGST 109

Db 103 TVGSSSSGGTNSGVSTNQCRISVTEHTKCDCIGRTT 138

Qy 16 CTPRNFSVSVREEL-KRTDTIFWPGCLVKRQGGNCACCLHNCNECCOPSKVTKVHEV 74

Db 46 CKPRDVTYVGLGEYPESTNLQVNPRCVTKVKGSG...CCNGDQICITAVETRNTTVVSV 102

Qy 75 IQLRPKTGVV-GLHKSTTDVALEHHEECDCVCRGST

RESULT 3

Matches 32; Conservative 14; Mismatches 41; Indels 12; Gaps 6;

Platelet-derived growth factor chain A1 precursor - rabbit

C;Species: *Orctolagus cuniculus* (domestic rabbit)

C;Date: 09-Oct-1992 #sequence\_revision 09-Oct-1992 #text\_change 27-Jun-1994

C;Accession: JS0735

R;Nakahara, K.; Nishimura, H.; Kuro-o, M.; Takewaki, S.; Iwase, M.; Ohkubo, A.; Yazaki, A.; Title: Identification of three types of PDGF-A chain gene transcripts in rabbit vascul

A;Reference number: JN0248; MUID:92246970

A;Accession: JS0735

A;Molecule type: mRNA

A;Residues: 1-198 <NAK>

A;Note: this protein corresponds to the endothelial type of human A chain

C;Superfamily: platelet-derived growth factor

F;1-20/Domain: signal sequence #status predicted <SIG>

F;21-89/Domain: propeptide #status predicted <PRO>

F;90-198/Product: platelet-derived growth factor A1 chain #status predicted <MAT>

Query Match 17.4%; Score 108; DB 2; Length 198;

Best Local Similarity 32.3%; Pred. No. 0.0016; Matches 32; Conservative 14; Mismatches 41; Indels 12; Gaps 6;

Db 98 CKTRVIVIEIPRSQDPTSANFLWPPCVEVKRTG--CC--NTSSVKCQPSRV--HH 149

Db 150 RSVKVAKEVVRKPK-LKEVQVRLLEHLECACASSAG 187

RESULT 4

151551

platelet-derived growth factor A chain short form precursor - African clawed frog

C;Species: *Xenopus laevis* (African clawed frog)

C;Accession: 151551

R;Mercola, M.; Melton, D.A.; Stiles, C.D.

Science 241, 1223-1225, 1988

A;Title: Platelet-derived growth factor A chain is maternally encoded in Xenopus embryos

A;Reference number: 151550; MUID:88321676

A;Accession: 151551

A;Status: preliminary; translated from GB/EMBL/DBBJ

A;Molecule type: mRNA

A;Residues: 1-200 <MER>

A;Cross-references: GB:M23238; NID:9214650; PIDN:AAA49928.1; PID:9214651

C;Superfamily: platelet-derived growth factor

Query Match 16.9%; Score 105; DB 2; Length 200;

Best Local Similarity 31.4%; Pred. No. 0.0032; Matches 33; Conservative 14; Mismatches 32; Indels 26; Gaps 8;

Db 101 CKTRVIVIEIPRSQDPTSANFLWPPCVEVKRTG--CC--NTSSVKCQPSRI--HH 152

Query 16 CTPRNFSVSI-REELKRTDIF-WPGCLVLRGGNCACCLHNCNECQCVPSKVTKYH 72

Db 101 CKTRVIVIEIPRSQDPTSANFLWPPCVEVKRTG--CC--NTSSVKCQPSRI--HH 152

Query 73 -----EVQLRPTGVGLHSLTDVALEHREECDCVCRGST 109

Db 153 RSVKVAKEVVRKPK-----LKEVL--VLEEEHLECTCTANS 190

RESULT 5

Matches 32; Conservative 14; Mismatches 41; Indels 12; Gaps 6;

Platelet-derived growth factor chain A precursor - African clawed frog

C;Species: *Xenopus laevis* (African clawed frog)

C;Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 16-Jul-1999

C;Accession: S08220

R;Bejcek, B.E.; Li, D.Y.; Deuel, T.F.

Nucleic Acids Res 18, 680, 1990

A;Title: Nucleotide sequence of a cDNA clone of *Xenopus* platelet-derived growth facto

A;Accession: S08220; MUID:90175018

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-215 <BEJ>

C;Cross-references: EMBL:X17545; NID:964973; PIDN:CAA35583.1; PID:964974

C;Keywords: alternative splicing; growth factor

F;1-22/Domain: propeptide #status predicted <SIG>

F;23-91/Domain: signal sequence #status predicted <PRO>

F;92-215/Product: platelet-derived growth factor chain A #status predicted <MAT>

Query Match 16.9%; Score 105; DB 2; Length 215;

Best Local Similarity 31.4%; Pred. No. 0.0034; Matches 33; Conservative 14; Mismatches 32; Indels 26; Gaps 8;

Db 101 CKTRVIVIEIPRSQDPTSANFLWPPCVEVKRTG--CC--NTSSVKCQPSRI--HH 152

Query 73 -----EVQLRPTGVGLHSLTDVALEHREECDCVCRGST 109

Db 153 RSVKVAKEVVRKPK-----LKEVL--VLEEEHLECTCTANS 190

RESULT 6

151550

platelet-derived growth factor A chain long form precursor - African clawed frog

C;Species: *Xenopus laevis* (African clawed frog)

C;Accession: 151550

R;Mercola, M.; Melton, D.A.; Stiles, C.D.

Science 241, 1223-1225, 1988

A;Title: Platelet-derived growth factor A chain is maternally encoded in Xenopus embr

A;Reference number: 151550

A;Status: preliminary; translated from GB/EMBL/DBBJ

A;Accession: 151550

A;Molecule type: mRNA

A;Residues: 1-226 <MER>

A;Cross-references: GB:M23237; NID:9214648; PIDN:AAA49927.1; PID:9214649

C;Superfamily: platelet-derived growth factor

Query Match 16.9%; Score 105; DB 2; Length 226;

Best Local Similarity 31.4%; Pred. No. 0.0035; Matches 33; Conservative 14; Mismatches 32; Indels 26; Gaps 8;

Db 101 CKTRVIVIEIPRSQDPTSANFLWPPCVEVKRTG--CC--NTSSVKCQPSRI--HH 152

Query 73 -----EVQLRPTGVGLHSLTDVALEHREECDCVCRGST 109

Db 153 RSVKVAKEVVRKPK-----LKEVL--VLEEEHLECTCTANS 190

RESULT 7

151551

platelet-derived growth factor chain B precursor [validated] - human transforming protein (

PFHUG2

platelet-derived growth factor chain B-chain; PDGF-B; PDGF-II; PDGF-related transforming protein (

N;Alternate names: PDGF B-chain; PDGF-B; PDGF-II; PDGF-related transforming protein (

C;Species: Homo Sapiens (man)

C;Date: 18-Apr-1984 #sequence\_revision 20-Sep-1984 #text\_change 08-Dec-2000  
 C;Accession: A94276; A21024; A23532; A93366; A25141; A93271; A93309; A43499; S56115; 157  
 R;Josephs, S.F.; Ratner, L.; Clarke, M.F.; Westin, E.H.; Reitz, M.S.; Wong-Staal, F.  
 Science 225, 636-639, 1984  
 A;Title: Transforming potential of human c-sis nucleotide sequences encoding platelet-derived growth factor 2 (PDGF)  
 A;Reference number: A94276; MUID:84250225  
 A;Molecule type: DNA  
 A;Residues: 1-241 <OS1>  
 A;Accession: A21024; MUID:84205633  
 A;Molecule type: DNA  
 A;Reference number: A21024; MUID:84205633  
 A;Cross-references: GB:K01401; NID:9338206; PIDN:AAA60552.1; PID:9338209  
 R;Chiue, I.M.; Reddy, E.P.; Givoli, D.; Robbins, K.C.; Tronick, S.R.; Aaronson, S.A.  
 Cell 37, 123-129, 1984  
 A;Residues: 17-20, 'RQ', 22-241 <CH1>  
 A;Cross-references: GB:K01917; NID:9338197  
 R;Rao, C.D.; Igarashi, H.; Chiu, I.M.; Robbins, K.C.; Aaronson, S.A.  
 Proc. Natl. Acad. Sci. U.S.A. 83, 2392-2396, 1986  
 A;Title: Structure and sequence of the human c-sis/platelet-derived growth factor 2 (PDGF)  
 A;Reference number: A23532; MUID:86205961  
 A;Accession: A23532  
 A;Molecule type: mRNA  
 A;Residues: 1-241 <RQ1>  
 A;Cross-references: GB: M12783; GB: M16288; NID:9338210; PIDN:AAA60553.1; PID:9338211  
 R;Collins, T.; Ginsburg, B.; Boss, J.M.; Orkin, S.H.; Pober, J.S.  
 Nature 316, 748-750, 1985  
 A;Title: Cultured human endothelial cells express platelet-derived growth factor B chain  
 A;Reference number: A93366; MUID:85396313  
 A;Accession: A93366  
 A;Molecule type: mRNA  
 A;Residues: 1-241 <COL>  
 A;Cross-references: GB:X02811; NID:935371; PIDN:CAA26579.1; PID:935372  
 R;Weich, H.A.; Sebald, W.; Schairer, H.U.; Hoppe, J.  
 FEBS Lett. 198, 344-348, 1986  
 A;Title: The human osteosarcoma cell line U-2 OS expresses a 3.8 kilobase mRNA which codes for a protein  
 A;Reference number: A25141; MUID:86164981  
 A;Accession: A25141  
 A;Molecule type: mRNA  
 A;Residues: 26-241 <RQ1>  
 A;Cross-references: GB:X03702; NID:935374; PIDN:CAA27333.1; PID:935375  
 R;Antoniades, H.N.; Hunkapiller, M.W.  
 Science 220, 963-965, 1983  
 A;Title: Human platelet-derived growth factor (PDGF): amino-terminal amino acid sequence  
 A;Reference number: A94271; MUID:83197379  
 A;Accession: A94271  
 A;Molecule type: protein  
 A;Residues: 82-100, 'E', 102-104, 'C', 106, 'C', 108-110 <ANT>  
 R;Waterfield, M.D.; Grace, G.T.; Whittle, N.; Stroobant, P.; Johnsson, A.; Wasteson, A.  
 Nature 304, 35-39, 1983  
 A;Title: Platelet-derived growth factor is structurally related to the putative transforming growth factor-  
 A;Reference number: A93308; MUID:83244981  
 A;Accession: A93308  
 A;Molecule type: protein  
 A;Residues: 82-112 <RAT>  
 R;Josephs, S.F.; Guo, C.; Ratner, L.; Wong-Staal, F.  
 Science 223, 487-491, 1984  
 A;Title: Human proto-oncogene nucleotide sequences corresponding to the transforming region  
 A;Reference number: A43499; MUID:84097555  
 A;Status: not compared with conceptual translation  
 A;Molecule type: DNA  
 A;Residues: 'O', 22-241 <J052>  
 R;Lu, K.V.; Rohde, M.F.; Thomason, A.R.; Kenney, W.C.; Lu, H.S.  
 Biochem. J. 309, 411-417, 1995  
 A;Title: Misreading of a TGA termination codon as tryptophan in recombinant platelet-derived growth factor  
 A;Reference number: S56115; MUID:95351967  
 A;Accession: S56115  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 82-93 <LUE>  
 R;Rao, C.D.; Pech, M.; Robbins, K.C.; Aaronson, S.A.

Mol. Cell. Biol. 8, 284-292, 1988  
 A;Title: The 5' untranslated sequence of the c-sis/platelet-derived growth factor 2 transcript  
 A;Reference number: 157635; MUID:88094398  
 A;Accession: I57635  
 A;Status: translated from GB/EMBL/DDBJ  
 A;Residues: 1-20 <RQ2>  
 A;Cross-references: GB: M19719; NID:9189727; PIDN:AAA60349.1; PID:9553608  
 R;Ratner, L.; Josephs, S.F.; Jarrett, R.; Reitz, M.S.  
 Nucleic Acids Res. 13, 5007-5018, 1985  
 A;Title: Nucleotide sequence of transforming human c-sis cDNA clones with homology to the human c-sis/platelet-derived growth factor 2 (PDGF)  
 A;Accession: I37266  
 A;Status: translated from GB/EMBL/DDBJ  
 A;Residues: 1-241 <RAT>  
 A;Cross-references: EMBL:X02744; NID:930246; PIDN:CAA26524.1; PID:930247  
 A;Title: The c-sis gene encodes a precursor of the B chain of platelet-derived growth factor  
 A;Reference number: A55030; MUID:84236121  
 A;Accession: A55030  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 'SLSL', 17-20, 'RQ', 22-241 <J041>  
 A;Cross-references: EMBL:X00556; GB:X00559; GB:X00560; GB:X00561; GB:X00562  
 R;Dirks, R.P.H.; Onnekink, C.; Jansen, H.J.; de Jong, A.; Bloemers, H.P.J.  
 Nucleic Acids Res. 23, 2815-2822, 1995  
 A;Title: A novel human c-sis mRNA species is transcribed from a promoter in c-sis intron 1  
 A;Reference number: S58382; MUID:95388493  
 A;Accession: S58383  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 'MFTMGL', 22-200 <DIR>  
 A;Cross-references: EMBL:X830505; NID:9951023; PIDN:CAA58679.1; PID:9951025  
 R;Cook, A.L.; Kirwin, P.M.; Craig, S.; Bowden, L.J.; Green, D.R.; Prise, M.J.; Richard Bloch, J. 281, 57-65, 1992  
 A;Title: Purification and analysis of proteinase-resistant mutants of recombinant platelet-derived growth factor B chain  
 A;Reference number: I38108; MUID:92117992  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: mRNA  
 A;Residues: 'M', 82-241 <COO>  
 A;Cross-references: EMBL:63966; NID:9311378; PIDN:CAA5383.1; PID:935377  
 A;Note: mutagenized recombinant sequence  
 C;Comment: Platelet-derived growth factor, a potent mitogen for cells of mesenchymal origin  
 A;Accession: I38108  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Gene: GDB:PDGFB  
 A;Cross-references: GDB:120709; OMIM:190040  
 A;Map position: 22q12.3-22q13.1  
 A;Introns: 5/3; 94/1; 19/23; 24/1  
 C;Complex: homodimer; heterodimer (see PIR:PFHUG1)  
 C;Superfamily: platelet-derived growth factor  
 C;Keywords: growth factor; mitogen  
 F:1-20/Domain: signal sequence #status predicted <SIG>  
 F:21-81/Domain: amino-terminal propeptide #status predicted <PRO>  
 F:82-190/Product: platelet-derived growth factor chain B #status experimental <MAT>  
 F:159-163/Region: receptor binding #status predicted  
 F:191-241/Domain: carboxy-terminal propeptide #status predicted <CTP>  
 F:97-141, 130-178, 134-180/disulfide bonds: #status experimental  
 F:124/Disulfide bonds: interchain (to 133 in homodimeric form) #status experimental  
 F:133/Disulfide bonds: interchain (to chain A-132 in heterodimeric form) #status experimental  
 F:133/Disulfide bonds: interchain (to chain A-124 in heterodimeric form) #status predicted  
 Query Match 16.9%; Score 105; DB: 1; Length: 241;  
 Best Local Similarity 33.3%; Pred. No. 0; 0037;  
 Matches 36; Conservative 12; Mismatches 34; Indels 26; Gaps 9;  
 Qy 7 LTEEVRLYSCIPRN-FSFSVIREELKRTDTIF-WPGCLYKRCGNCACCLHNCNECOC 62  
 F: 82-93 <LUE>  
 Db 88 IAPAMIAECKTRTEVFEIS-RRLIDRTNANFLVWPPCVCVORCSG--CC--NNRNQVQ 141



Db 107 ::::| | : : ::| | ::| 107 MRKPHOG----QHIGEMSFLQHNCCEC 130

RESULT 10

B28964 platelet-derived growth factor chain A precursor splice form 2 - human

C;Species: Homo sapiens (man)

C;Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 16-Jul-1999

C;Accession: B28964; B42002; B28122

R;Bonhron, D.T.; Morton, C.C.; Orkin, S.H.; Collins, T.

Proc. Natl. Acad. Sci. U.S.A., 85, 1491-1496, 1988

A;Title: Platelet-derived growth factor A chain: gene structure, chromosomal location, and

A;Reference number: A28964; MUID:8814463

A;Cross-references: EMBL:24120

A;Superfamily: platelet-derived growth factor C;Keywords: growth factor; mitogen; platelet

A;Accession: B42002; MUID:92307656

A;Title: platelet-derived growth factor A chain: confirmation of localization of PDGF-A

A;Accession: B42002; MUID:92307656

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 152-196 <BO2>

R;Norsman, F.; Bwayater, M.; Knott, T.J.; Scott, J.; Betsholtz, C.

Mol. Cell. Biol. 8, 571-577, 1988

A;Title: Structural characterization of the human platelet-derived growth factor A-chain

A;Reference number: A28122; MUID:88144698

A;Accession: B28122

R;Bonhron, D.T.; Morton, C.C.; Orkin, S.H.; Collins, T.

A;Molecule type: mRNA

A;Residues: 1-63, <TRD>, 67-196 <ROR>

A;Cross-references: GB:M20488

A;Note: the authors translated the codon AGA for residue 64 as Arg, CGT for residue 65 as

C;Comment: Exon 6 is spliced out of this variant splice form. For the major splice form

A;Gene: GB:PDGFA

A;Cross-references: GDB:120266; OMIM:173430

A;Map position: 7p22-p22

C;Superfamily: platelet-derived growth factor

C;Keywords: alternative splicing; glycoprotein; growth factor; mitogen; platelet

Query Match 16.7%; Score 104; DB 2; Length 197;

Best Local Similarity 34.0%; Pred. No. 0.0039; Matches 32; Conservative 12; Mismatches 34; Indels 16; Gaps 6;

Query 16 CTPRNFSVSI-REELKRDTIF--WPGCLLVLKRCGGNCACCLUNCNFCQCVPSKV--TK 69

Db 89 CKRTIVVIEIPRSQVDTTSANFLWIPPCVEVKRTG--CC--NTSSVKCOPSRVHRSV 143

QY 70 KYHEVLOQPKPGVYRGGLKSLDVALEHHNEECDC 103

Db 144 KVAKVEYVVRKKPKLKEV---QVRLEEHLECAC 172

RESULT 12

PFHUG1

platelet-derived growth factor chain A precursor - human

A;Alternate names: PDGF A-chain; PDGF-A; platelet-derived growth factor 1

C;Species: Homo sapiens (man)

C;Date: 04-Dec-1986 #sequence\_revision 04-Dec-1986 #text\_change 18-Feb-2000

C;Accession: A28964; 547564; A42002; A01379; S00173; A28122

R;Bonhron, D.T.; Morton, C.C.; Orkin, S.H.; Collins, T.

Proc. Natl. Acad. Sci. U.S.A., 85, 1492-1496, 1988

A;Title: Platelet-derived growth factor A chain: gene structure, chromosomal location

A;Reference number: A28964; MUID:8814463

A;Accession: A28964; MUID:94312450

A;Molecule type: DNA

A;Residues: 1-211 <BO2>

A;Cross-references: GB:M21571; GB:J03638; GB:M19984; GB:M19985; GB:M19986; GB:M19987;

R;Akimoto, Y.; Kuramoto, A.

Biochim. Biophys. Acta 1222, 511-514, 1994

A;Title: Gene regulation by the 5'-untranslated region of the platelet-derived growth

A;Reference number: S47564; MUID:94312450

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-21 <TRK>

R;Bonhron, D.; Collins, T.; Grzeschik, K.H.; van Roy, N.; Speleman, F.

Genomics 13, 257-263, 1992

A;Title: Platelet-derived growth factor A chain: confirmation of localization of PDGF

A;Reference number: A42002; MUID:92307656

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 152-211 <BO2>

R;Betsholtz, C.; Johnson, A.; Heldin, C.H.; Westermark, B.; Lind, P.; Urdea, M.S.; E

Nature 320, 695-699, 1986

A;Title: cDNA sequence and chromosomal localization of human platelet-derived growth

A;Reference number: A01379; MUID:86203630

A;Accession: A01379

A;Molecule type: mRNA

A;Residues: 1-211 <BBT>

C;Species: Rattus norvegicus (Norway rat)

C;Date: 07-Apr-1994 #sequence\_revision 07-Apr-1994 #text\_change 16-Jul-1999

C;Accession: S25056; S33764

R;Harren, B.; Weyer, K.A.; Rouge, M.; Loetscher, P.; Pech, M.

Submitted to the EMBL Data Library, July 1992

A;Description: Cross-species conservation in sequence and function of PDGF ligands and r

A;Reference number: S25096

A;Accession: S25096

A;Molecule type: mRNA

A;Residues: 1-197 <HER1>

C;Cross-references: EMBL:21120; NID:956865; PIDN:CAA78490.1; PID:956866

R;Bierren, B.; Weyer, K.A.; Rouge, M.; Loetscher, P.; Pech, M.

Biochim. Biophys. Acta 1173, 294-302, 1993





Best Local Similarity	100.0%	Pred.	No.	1.4e-63
Matches	111;	Conservative	0;	Mismatches
RESULT	2	PRELIMINARY;	PRT;	345 AA.
ID	09NRA1			
AC	09NRA1;	PRELIMINARY;	PRT;	345 AA.
DT	01-OCT-2000 (TREMBLREL. 15, Created)			
DT	01-MAR-2001 (TREMBLREL. 15, Last sequence update)			
DE	PLATELET-DERIVED GROWTH FACTOR C.			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TAXID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=LUNG;			
RA	Li X., Ponten A., Kase K., Karlsson L., Abramsson A., Uutela M., Backstrom G., Hellstrom M., Boston H., Li H., Soriano P., Bettcholtz C., Heijnen C.-H., Alitalo K., Ostman A., Eriksson U. "PDGF-C is a novel protease-activated ligand for the PDGF alpha receptor"; Cell Biol. 0-0-0(2000).			
RL	Nat. Cell Biol. 0-0-0(2000).			
DR	EMBL: AF24813; AAC80597.1; -.			
DR	InterPro: IPR000072; -.			
DR	InterPro: IPR000839; -.			
DR	Pfam: PF00341; PDGF_1;			
DR	PROSITE: PS01180; CUB_1;			
DR	PROSITE: PS50278; PDGF_2; 1.			
DR	SMART: SM00012; CUB_1;			
SQ	SEQUENCE 345 AA; 39043 MN; 590889CEA55CC5EA CRC64;			
Query Match	100.0%	Score	631;	DB 4;
Best Local Similarity	100.0%	Pred.	No.	1.4e-63;
Matches	111;	Conservative	0;	Mismatches
RESULT	3	PRELIMINARY;	PRT;	345 AA.
ID	09QY71			
AC	09QY71;	PRELIMINARY;	PRT;	345 AA.
DT	01-MAY-2000 (TREMBLREL. 13, Created)			
DT	01-MAY-2000 (TREMBLREL. 13, Last sequence update)			
DE	FALLOTOGEN.			
OS	Mus musculus (Mouse)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TAXID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=SWISS-WEBSTER/NIH;			
RA	Ding H., Wu X., Kim I., Tam P.P.L., Koh G.Y., Nagy A.; "The mouse pdgf gene: Dynamic expression in embryonic tissues during organogenesis"; J. Mech. Dev. 0-0-0(2000)			
RL	DRB: AF28675; AAC91463.1; -.			
DR	InterPro: IPR000072; -.			
DR	InterPro: IPR000839; -.			
DR	Pfam: PF00431; CUB_1;			
DR	PROSITE: PS01180; CUB_1;			
DR	PROSITE: PS50278; PDGF_2; 1.			
DR	SMART: SM00042; CUB_1;			
SQ	SEQUENCE 345 AA; 38886 MN; FA1486BED6D362F8 CRC64;			
Query Match	94.0%	Score	584;	DB 11;
Best Local Similarity	92.8%	Pred.	No.	2.5e-59;
Matches	103;	Conservative	4;	Mismatches
RESULT	4	PRELIMINARY;	PRT;	345 AA.
ID	09JH8			
AC	09JH8;	PRELIMINARY;	PRT;	345 AA.
DT	01-OCT-2000 (TREMBLREL. 15, Created)			
DT	01-MAR-2001 (TREMBLREL. 15, Last sequence update)			
DE	PLATELET-DERIVED GROWTH FACTOR C.			
OS	Mus musculus (Mouse)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TAXID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=SWISS-WEBSTER/NIH;			
RA	Ding H., Wu X., Kim I., Tam P.P.L., Koh G.Y., Nagy A.; "The mouse pdgf gene: Dynamic expression in embryonic tissues during organogenesis"; J. Mech. Dev. 0-0-0(2000)			
RL	DRB: AF28675; AAC91463.1; -.			
DR	InterPro: IPR000072; -.			
DR	InterPro: IPR000839; -.			
DR	Pfam: PF00431; CUB_1;			
DR	PROSITE: PS01180; CUB_1;			
DR	PROSITE: PS50278; PDGF_2; 1.			
DR	SMART: SM00042; CUB_1;			
SQ	SEQUENCE 345 AA; 38886 MN; FA1486BED6D362F8 CRC64;			
Query Match	94.0%	Score	584;	DB 11;
Best Local Similarity	92.8%	Pred.	No.	2.5e-59;
Matches	103;	Conservative	4;	Mismatches
RESULT	5	PRELIMINARY;	PRT;	345 AA.
ID	09EOX6			
AC	09EOX6;	PRELIMINARY;	PRT;	345 AA.
DT	01-MAR-2001 (TREMBLREL. 15, Created)			

Db	295	QCIPKVKYHEVILKPRSGVRLHSKLTIDVPEHRECCDVCKGNSG	345
RESULT	7		
Q9GZ0			
ID	09GZ0	PRELIMINARY;	PRT; 370 AA.
OGGZ0			
AC	09GZ0;		
DT	01-MAR-2001 (TREMBLEL 16, Last sequence update)		
DT	01-MAR-2001 (TREMBLEL 16, Created)		
DT	01-MAR-2001 (TREMBLEL 16, Last sequence update)		
DT	01-MAR-2001 (TREMBLEL 16, Last sequence update)		
DE	SPINAL CORD-DERIVED GROWTH FACTOR-B (MSTP036).		
GN	HSCDF-B.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
RN	NCBI_TaxID=10116;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-WISTAR; TISSUE-KIDNEY;		
RA	Hamada T., Ul-Tei K., Imaki J., Miyata Y.;		
RA	"Molecular Cloning of SCDGF-B, a Novel Growth Factor Homologous to		
RA	SCDGF/PDG-C/fallostein";		
RA	Biochem. Biophys. Res. Commun. 0:0-0(2000).		
DR	EMBL; AB013930; BAB19869_1; -.		
SQ	SEQUENCE 345 AA; 38734 MW; F296DA6E9B765D10 CRC64;		
RESULT	6		
Q9J946			
AC	09J946;	PRELIMINARY;	PRT; 345 AA.
DT	01-OCT-2000 (TREMBLEL 15, Created)		
DT	01-OCT-2000 (TREMBLEL 15, Last sequence update)		
DE	SPINAL CORD-DERIVED GROWTH FACTOR.		
GN	SCDGF.		
OS	Gallus gallus (Chicken).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Archosauria; Aves; Neognathae; Galiformes; Phasianidae; Phasianinae;		
OC	NCBI_TaxID=9031;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-WHITE LEGHORN; TISSUE-SPINAL CORD;		
RX	MEDLINE-20317014; PubMed=1058496;		
RA	Hamada T., Ul-Tei K., Miyata Y.		
RT	"A novel gene derived from developing spinal cords, SCDGF, is a unique		
RT	member of the PDGF/VEGF family.";		
RL	FEMS Lett. 475:97-102(2000).		
EMBL;	AB033809; BAB03265_1; -.		
DR	InterPro: IPRO00072; -.		
DR	InterPro: IPRO00859; -.		
DR	Pfam: PF00431; CUB_1.		
DR	PROSITE: PS01180; CUB_1.		
DR	PROSITE: PS50778; PDGF_2; 1.		
DR	SMART: SM00042; CUB_1.		
SQ	SEQUENCE 345 AA; 38940 MW; 97ACEA992BF5128C CRC64;		
RESULT	8		
Q9EQT1			
ID	09EQT1	PRELIMINARY;	PRT; 370 AA.
OGEQT1			
AC	09EQT1;		
DT	01-MAR-2001 (TREMBLEL 16, Created)		
DT	01-MAR-2001 (TREMBLEL 16, Last sequence update)		
DT	01-MAR-2001 (TREMBLEL 16, Last sequence update)		
DE	SPINAL-CORD DERIVED GROWTH FACTOR-B.		
GN	RSCDGF-B.		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OX	NCBI_TaxID=10116;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Hamada T., Ul-Tei K., Imaki J., Miyata Y.;		
RA	"Molecular Cloning of SCDGF-B, a Novel Growth Factor Homologous to		
RA	SCDGF/PDG-C/fallostein";		
RA	Biochem. Biophys. Res. Commun. 0:0-0(2000).		
DR	EMBL; AB022170; BAB18920_1; -.		
SQ	SEQUENCE 370 AA; 42809 MW; 7BE8A251679BF73 CRC64;		
Query Match	51.3%	Score 318.5;	DB 11; Length 370;
Query Match	88.7%	Score 551;	DB 13; Length 345;
Best Local Similarity	86.5%	Pred NO. 1.6e-55;	
Matches	96;	Conservative 9;	Mismatches 6;
Indels	0;	Gaps 0;	
Q9	1	WVDLNLTTEEVRLYSCTPRNFSVIREELKRTDIFWPCCLVYKRCGGNCACCLHNCNSC	60
Db	235	WVDLNLTKEVRLYSCTPRNFSVIREELKRTDIFWPCCLVYKRCGGNCACCHONCNEC	294
QY	61	QCPSVKVKYHEVILQLRKPRTGFLGLHKSITDVALEHHBECDCVCKGNSG	111



RA	Alitalo O., Stacker S.A.:	OY	75 LQLRPKTVGRGLHKSLTDALEHHHECDC 103
RT	"Vascular endothelial growth factor D ('VEGF-D') is a ligand for the tyrosine kinases VEGF receptor 2 (Flk1) and VEGF 'receptor 3 (Flt4).";	RT	::::  :  :  :  :  :  :  :  :
RL	Proc. Natl. Acad. Sci. U.S.A. 95:548-553(1998).	RL	107 MKIKPH---ISQHIMDMSFQHSQEC 130
DR		DR	
EMBL; Y12864; CAA73371.1; JOINED.	EMBL; Y12866; CAA73371.1; JOINED.	EMBL; Y12867; CAA73371.1; JOINED.	EMBL; Y12868; CAA73371.1; JOINED.
DR		DR	
EMBL; Y12869; CAA73371.1; JOINED.	EMBL; Y12870; CAA73371.1; JOINED.	EMBL; Y12871; CAA73371.1; JOINED.	EMBL; Y12872; CAA73371.1; JOINED.
DR		DR	
EMBL; AJ000185; CAA03942.1; -.	EMBL; AJ000185; CAA03942.1; -.	EMBL; Y12873; CAA73370.1; -.	EMBL; Y12874; CAA73370.1; -.
DR		DR	
HSSP; P15692; IVEP;	HSSP; P15692; IVEP;	DR	
DR		DR	
InterPro; IPR000072; -.	InterPro; IPR000072; -.	InterPro; IPR000072; -.	InterPro; IPR000072; -.
DR		DR	
Pfam; PF00341; PDGF; 1.	Pfam; PF00341; PDGF; 1.	Pfam; PF00341; PDGF; 1.	Pfam; PF00341; PDGF; 1.
DR		DR	
PROSITE; PS50249; PDGF_1; 1.	PROSITE; PS50249; PDGF_1; 1.	PROSITE; PS50278; PDGF_2; 1.	PROSITE; PS50278; PDGF_2; 1.
DR		DR	
SMART; SM00141; PDGF; 1.	SMART; SM00141; PDGF; 1.	SMART; SM00141; PDGF; 1.	SMART; SM00141; PDGF; 1.
SQ	SEQUENCE 354 AA; 4044 MW; 2048D769b735173E CRC64;	SQ	SEQUENCE 354 AA; 4044 MW; 2048D769b735173E CRC64;
RESULT 12	Query Match 18.6%; Score 115.5; DB 4; Length 354; Best Local Similarity 33.0%; Pred. No. 042571; Mismatches 34; Indels 11; Gaps 5; Matches 34; Conservative	RESULT 13	Query Match 17.5%; Score 108.5; DB 13; Length 194; Best Local Similarity 25.8%; Pred. No. 042572; Mismatches 23; Indels 11; Gaps 4; Matches 23; Conservative
O42571	PRELIMINARY; PRT; 148 AA.	O42572	PRELIMINARY; PRT; 194 AA.
ID		ID	
AC	042571; 01-JAN-1998 (TREMBLrel. 05, Created)	AC	042572; 01-JAN-1998 (TREMBLrel. 05, Created)
DT	01-JAN-1998 (TREMBLrel. 05, Last sequence update)	DT	01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT	01-MAR-2001 (TREMBLrel. 16, Last annotation update)	DT	01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE	VEGFR	DE	VEGFR
GN		GN	
Xenopus laevis (African clawed frog)	Xenopus laevis (African clawed frog)	Xenopus laevis (African clawed frog)	Xenopus laevis (African clawed frog)
OS		OS	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Xenopus; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopidae; Xenopus.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Xenopus; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopidae; Xenopus.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Xenopus; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopidae; Xenopus.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Xenopus; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopidae; Xenopus.
RA	SEQUENCE FROM N.A.	RA	SEQUENCE FROM N.A.
RL	Cleaver O., Tonissen K.F., Saha M.S., Krieg P.A.; Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.	RL	Cleaver O., Tonissen K.F., Saha M.S., Krieg P.A.; Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR		DR	
EMBL; AF005594; AAB63680.1; -.	EMBL; AF005594; AAB63680.1; -.	EMBL; AF005593; AAB63679.1; -.	EMBL; AF005593; AAB63679.1; -.
DR		DR	
HSSP; P15692; IVEP;	HSSP; P15692; IVEP;	DR	
DR		DR	
InterPro; IPR000072; -.	InterPro; IPR000072; -.	InterPro; IPR000072; -.	InterPro; IPR000072; -.
DR		DR	
Pfam; PF00341; PDGF; 1.	Pfam; PF00341; PDGF; 1.	Pfam; PF00341; PDGF; 1.	Pfam; PF00341; PDGF; 1.
DR		DR	
PROSITE; PS50249; PDGF_1; 1.	PROSITE; PS50249; PDGF_1; 1.	PROSITE; PS50278; PDGF_2; 1.	PROSITE; PS50278; PDGF_2; 1.
DR		DR	
SMART; SM00141; PDGF; 1.	SMART; SM00141; PDGF; 1.	SMART; SM00141; PDGF; 1.	SMART; SM00141; PDGF; 1.
SQ	SEQUENCE 194 AA; 2267 MW; 85D7BEC7CBFEF17E CRC64;	SQ	SEQUENCE 194 AA; 2267 MW; 85D7BEC7CBFEF17E CRC64;
RESULT 14	Query Match 17.5%; Score 108.5; DB 13; Length 194; Best Local Similarity 25.8%; Pred. No. 015354; Mismatches 34; Indels 11; Gaps 4; Matches 23; Conservative	RESULT 14	Query Match 17.5%; Score 108.5; DB 13; Length 194; Best Local Similarity 25.8%; Pred. No. 015354; Mismatches 34; Indels 11; Gaps 4; Matches 23; Conservative
O15354	PRELIMINARY; PRT; 185 AA.	O15354	PRELIMINARY; PRT; 185 AA.
ID		ID	
AC	015354; 01-NOV-1996 (TREMBLrel. 01, Created)	AC	015354; 01-NOV-1996 (TREMBLrel. 01, Created)
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)	DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT	01-MAR-2001 (TREMBLrel. 16, Last annotation update)	DT	01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE	C-SIS PROTO-OONECONE (FRAGMENT).	DE	C-SIS PROTO-OONECONE (FRAGMENT).
OS	Homo sapiens (Human).	OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Xenopus; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopidae; Xenopus.	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Xenopus; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopidae; Xenopus.
OX	NCBI_TaxID:9606;	OX	NCBI_TaxID:9606;
RN	SEQUENCE FROM N.A.	RN	SEQUENCE FROM N.A.
RC	TISSUE-CHORIOCARCINOMA;	RC	TISSUE-CHORIOCARCINOMA;
RX	MEDLINE=95388493; PubMed=7659502;	RX	MEDLINE=95388493; PubMed=7659502;
RT	"A novel human C-SIS mRNA species is transcribed from a promoter in c-sis intron 1 and contains the code for an alternative PDGF B-like protein.";	RT	"A novel human C-SIS mRNA species is transcribed from a promoter in c-sis intron 1 and contains the code for an alternative PDGF B-like protein.";
RT	Nucleic Acids Res. 23:2815-2822(1995).	RT	Nucleic Acids Res. 23:2815-2822(1995).
RL		RL	
EMBL; X83705; CAA58679.1; -.	EMBL; X83705; CAA58679.1; -.	EMBL; X83705; CAA58679.1; -.	EMBL; X83705; CAA58679.1; -.
DR		DR	
InterPro; IPR000072; -.	InterPro; IPR000072; -.	InterPro; IPR000072; -.	InterPro; IPR000072; -.
DR		DR	
Pfam; PF00341; PDGF; 1.	Pfam; PF00341; PDGF; 1.	Pfam; PF00341; PDGF; 1.	Pfam; PF00341; PDGF; 1.
DR		DR	
PROSITE; PS50249; PDGF_1; 1.	PROSITE; PS50249; PDGF_1; 1.	PROSITE; PS50278; PDGF_2; 1.	PROSITE; PS50278; PDGF_2; 1.
DR		DR	
SMART; SM00141; PDGF; 1.	SMART; SM00141; PDGF; 1.	SMART; SM00141; PDGF; 1.	SMART; SM00141; PDGF; 1.
SQ	SEQUENCE 148 AA; 17234 MW; 4AD153CA2F8B1E95 CRC64;	SQ	SEQUENCE 148 AA; 17234 MW; 4AD153CA2F8B1E95 CRC64;
RESULT 15	Query Match 17.5%; Score 108.5; DB 13; Length 148; Best Local Similarity 25.8%; Pred. No. 015355; Mismatches 34; Indels 11; Gaps 4; Matches 23; Conservative	RESULT 15	Query Match 17.5%; Score 108.5; DB 13; Length 148; Best Local Similarity 25.8%; Pred. No. 015355; Mismatches 34; Indels 11; Gaps 4; Matches 23; Conservative
O15355	PRELIMINARY; PRT; 185 AA.	O15355	PRELIMINARY; PRT; 185 AA.
ID		ID	
AC	015355; 01-NOV-1996 (TREMBLrel. 01, Created)	AC	015355; 01-NOV-1996 (TREMBLrel. 01, Created)
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)	DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT	01-MAR-2001 (TREMBLrel. 16, Last annotation update)	DT	01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE	C-SIS PROTO-OONECONE (FRAGMENT).	DE	C-SIS PROTO-OONECONE (FRAGMENT).
OS	Homo sapiens (Human).	OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Xenopus; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopidae; Xenopus.	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Xenopus; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopidae; Xenopus.
OX	NCBI_TaxID:9606;	OX	NCBI_TaxID:9606;
RN	SEQUENCE FROM N.A.	RN	SEQUENCE FROM N.A.
RC	TISSUE-CHORIOCARCINOMA;	RC	TISSUE-CHORIOCARCINOMA;
RX	MEDLINE=95388493; PubMed=7659502;	RX	MEDLINE=95388493; PubMed=7659502;
RT	"A novel human C-SIS mRNA species is transcribed from a promoter in c-sis intron 1 and contains the code for an alternative PDGF B-like protein.";	RT	"A novel human C-SIS mRNA species is transcribed from a promoter in c-sis intron 1 and contains the code for an alternative PDGF B-like protein.";
RT	Nucleic Acids Res. 23:2815-2822(1995).	RT	Nucleic Acids Res. 23:2815-2822(1995).
RL		RL	
EMBL; X83705; CAA58679.1; -.	EMBL; X83705; CAA58679.1; -.	EMBL; X83705; CAA58679.1; -.	EMBL; X83705; CAA58679.1; -.
DR		DR	
InterPro; IPR000072; -.	InterPro; IPR000072; -.	InterPro; IPR000072; -.	InterPro; IPR000072; -.
DR		DR	
Pfam; PF00341; PDGF; 1.	Pfam; PF00341; PDGF; 1.	Pfam; PF00341; PDGF; 1.	Pfam; PF00341; PDGF; 1.
DR		DR	
PROSITE; PS50249; PDGF_1; 1.	PROSITE; PS50249; PDGF_1; 1.	PROSITE; PS50278; PDGF_2; 1.	PROSITE; PS50278; PDGF_2; 1.
DR		DR	
SMART; SM00141; PDGF; 1.	SMART; SM00141; PDGF; 1.	SMART; SM00141; PDGF; 1.	SMART; SM00141; PDGF; 1.
SQ	SEQUENCE 148 AA; 17234 MW; 4AD153CA2F8B1E95 CRC64;	SQ	SEQUENCE 148 AA; 17234 MW; 4AD153CA2F8B1E95 CRC64;
RESULT 16	Query Match 17.5%; Score 108.5; DB 13; Length 148; Best Local Similarity 25.8%; Pred. No. 015356; Mismatches 34; Indels 11; Gaps 4; Matches 23; Conservative	RESULT 16	Query Match 17.5%; Score 108.5; DB 13; Length 148; Best Local Similarity 25.8%; Pred. No. 015356; Mismatches 34; Indels 11; Gaps 4; Matches 23; Conservative
O15356	PRELIMINARY; PRT; 185 AA.	O15356	PRELIMINARY; PRT; 185 AA.
ID		ID	
AC	015356; 01-NOV-1996 (TREMBLrel. 01, Created)	AC	015356; 01-NOV-1996 (TREMBLrel. 01, Created)
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)	DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT	01-MAR-2001 (TREMBLrel. 16, Last annotation update)	DT	01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE	C-SIS PROTO-OONECONE (FRAGMENT).	DE	C-SIS PROTO-OONECONE (FRAGMENT).
OS	Homo sapiens (Human).	OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Xenopus; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopidae; Xenopus.	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Xenopus; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopidae; Xenopus.
OX	NCBI_TaxID:9606;	OX	NCBI_TaxID:9606;
RN	SEQUENCE FROM N.A.	RN	SEQUENCE FROM N.A.
RC	TISSUE-CHORIOCARCINOMA;	RC	TISSUE-CHORIOCARCINOMA;
RX	MEDLINE=95388493; PubMed=7659502;	RX	MEDLINE=95388493; PubMed=7659502;
RT	"A novel human C-SIS mRNA species is transcribed from a promoter in c-sis intron 1 and contains the code for an alternative PDGF B-like protein.";	RT	"A novel human C-SIS mRNA species is transcribed from a promoter in c-sis intron 1 and contains the code for an alternative PDGF B-like protein.";
RT	Nucleic Acids Res. 23:2815-2822(1995).	RT	Nucleic Acids Res. 23:2815-2822(1995).
RL		RL	
EMBL; X83705; CAA58679.1; -.	EMBL; X83705; CAA58679.1; -.	EMBL; X83705; CAA58679.1; -.	EMBL; X83705; CAA58679.1; -.
DR		DR	
InterPro; IPR000072; -.	InterPro; IPR000072; -.	InterPro; IPR000072; -.	InterPro; IPR000072; -.
DR		DR	
Pfam; PF00341; PDGF; 1.	Pfam; PF00341; PDGF; 1.	Pfam; PF00341; PDGF; 1.	Pfam; PF00341; PDGF; 1.
DR		DR	
PROSITE; PS50249; PDGF_1; 1.	PROSITE; PS50249; PDGF_1; 1.	PROSITE; PS50278; PDGF_2; 1.	PROSITE; PS50278; PDGF_2; 1.
DR		DR	
SMART; SM00141; PDGF; 1.	SMART; SM00141; PDGF; 1.	SMART; SM00141; PDGF; 1.	SMART; SM00141; PDGF; 1.
SQ	SEQUENCE 148 AA; 17234 MW; 4AD153CA2F8B1E95 CRC64;	SQ	SEQUENCE 148 AA; 17234 MW; 4AD153CA2F8B1E95 CRC64;
RESULT 17	Query Match 17.5%; Score 108.5; DB 13; Length 148; Best Local Similarity 25.8%; Pred. No. 015357; Mismatches 34; Indels 11; Gaps 4; Matches 23; Conservative	RESULT 17	Query Match 17.5%; Score 108.5; DB 13; Length 148; Best Local Similarity 25.8%; Pred. No. 015357; Mismatches 34; Indels 11; Gaps 4; Matches 23; Conservative
O15357	PRELIMINARY; PRT; 185 AA.	O15357	PRELIMINARY; PRT; 185 AA.
ID		ID	
AC	015357; 01-NOV-1996 (TREMBLrel. 01, Created)	AC	015357; 01-NOV-1996 (TREMBLrel. 01, Created)
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)	DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT	01-MAR-2001 (TREMBLrel. 16, Last annotation update)	DT	01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE	C-SIS PROTO-OONECONE (FRAGMENT).	DE	C-SIS PROTO-OONECONE (FRAGMENT).
OS	Homo sapiens (Human).	OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Xenopus; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopidae; Xenopus.	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Xenopus; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopidae; Xenopus.
OX	NCBI_TaxID:9606;	OX	NCBI_TaxID:9606;
RN	SEQUENCE FROM N.A.	RN	SEQUENCE FROM N.A.
RC	TISSUE-CHORIOCARCINOMA;	RC	TISSUE-CHORIOCARCINOMA;
RX	MEDLINE=95388493; PubMed=7659502;	RX	MEDLINE=95388493; PubMed=7659502;
RT	"A novel human C-SIS mRNA species is transcribed from a promoter in c-sis intron 1 and contains the code for an alternative PDGF B-like protein.";	RT	"A novel human C-SIS mRNA species is transcribed from a promoter in c-sis intron 1 and contains the code for an alternative PDGF B-like protein.";
RT	Nucleic Acids Res. 23:2815-2822(1995).	RT	Nucleic Acids Res. 23:2815-2822(1995).
RL		RL	
EMBL; X83705; CAA58679.1; -.	EMBL; X83705; CAA58679.1; -.	EMBL; X83705; CAA58679.1; -.	EMBL; X83705; CAA58679.1; -.
DR		DR	
InterPro; IPR000072; -.	InterPro; IPR000072; -.	InterPro; IPR000072; -.	InterPro; IPR000072; -.
DR		DR	
Pfam; PF00341; PDGF; 1.	Pfam; PF00341; PDGF; 1.	Pfam; PF00341; PDGF; 1.	Pfam; PF00341; PDGF; 1.
DR		DR	
PROSITE; PS50249; PDGF_1; 1.	PROSITE; PS50249; PDGF_1; 1.	PROSITE; PS50278; PDGF_2; 1.	PROSITE; PS50278; PDGF_2; 1.
DR		DR	
SMART; SM00141; PDGF; 1.	SMART; SM00141; PDGF; 1.	SMART; SM00141; PDGF; 1.	SMART; SM00141; PDGF; 1.
SQ	SEQUENCE 148 AA; 17234 MW; 4AD153CA2F8B1E95 CRC64;	SQ	SEQUENCE 148 AA; 17234 MW; 4AD153CA2F8B1E95 CRC64;

SQ	SEQUENCE	207 AA:	21602 MW:	EDB4B1C0DFDAD6BC CRC64:
PROSIE; P50249; PDGF-1; 1.				
PROSIE; P50278; PDGF-2; 1.				
SMART; SM00141; PDGF; 1.				
NON-TER 185	185			
SEQUENCE 185 AA:	20774 MW:	A2BC585F88DFFEE59	CRC64:	
Query Match 16.9%: Score 105; DB 4; Length 185;				
Best Local Similarity 33.3%; Pred. No. 0.00021; Mismatches 36; Conservative 12; Indels 26; Gaps 9; Matches 27;				
Query Match 16.9%: Score 105; DB 4; Length 207;				
Best Local Similarity 30.0%; Pred. No. 0.00023; Mismatches 34; Conservative 17; Indels 12; Gaps 4; Matches 27;				
Query 15 SCTPRNFSVSIRESLKR-DTIFWPGCLVKRQGNCNACCLHNNECQVPSKVKRKHIE 73				
Db 46 TCQPREVNPVPLTVELMGTVAKQLYPSVQRCG--CCPD- DGLECVPTGQHQVRM 100				
Query 74 VLOQRPKTVGVRGLHKSLSIVALEHHHECDC 103				
Db 101 ILMIRYPS-----SOLGENSLEHHSOC 124				
73 IAPAMIAECKTRTEVFEIS-RKLIDRTNANFLWMPVCEVORCSG--CC--NNRNVOC 126				
63 VPSKVVKVVKYHEVQLRP---KTVG---RGLMSLTDVALEHHECDC 103				
127 RPTQV-----QLRQVQVRKIEIVRKPKPIKKAT-WTLEDHLACKC 165				